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                  GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on:    March  5, 2006, 08:22:14 ; Search time 275 Seconds
                                       (without alignments)
                                       5371.468 Million cell updates/sec

Title:          US-10-658-482-1
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Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters:    2606114

Minimum DB seq length: 0
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Post-processing:  Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	Query Match %	Length	DB	ID	Description
c	1	42.4	5.1	9007	3	US-09-902-540-908	Sequence 908, App
	2	38	4.6	364	3	US-09-621-976-17202	Sequence 17202, A
	3	36.8	4.4	1335	3	US-09-902-540-5256	Sequence 5256, Ap
c	4	36.8	4.4	34316	3	US-09-902-540-1257	Sequence 1257, Ap
	5	36	4.3	993	3	US-09-154-750A-69	Sequence 69, Appl
	6	35.8	4.3	1038	3	US-09-902-540-3643	Sequence 3643, Ap
c	7	35.8	4.3	19269	3	US-09-902-540-1175	Sequence 1175, Ap
	8	35.8	4.3	26729	3	US-10-283-247-6	Sequence 6, Appli
	9	35.8	4.3	70383	3	US-10-283-247-3	Sequence 3, Appli
	10	35.4	4.3	3153	3	US-09-922-501-13	Sequence 13, Appl
c	11	35.2	4.2	505	3	US-09-621-976-15639	Sequence 15639, A
c	12	35	4.2	569	3	US-09-561-077C-53	Sequence 53, Appl
	13	35	4.2	601	3	US-09-949-016-45047	Sequence 45047, A
	14	35	4.2	2662	3	US-09-774-528-94	Sequence 94, Appl
	15	35	4.2	2662	3	US-10-120-988-94	Sequence 94, Appl
	16	35	4.2	5275	3	US-09-561-077C-59	Sequence 59, Appl
c	17	34.8	4.2	825	3	US-09-902-540-7038	Sequence 7038, Ap
c	18	34.8	4.2	4152	3	US-09-081-385-5	Sequence 5, Appli
c	19	34.8	4.2	4152	3	US-09-752-639-5	Sequence 5, Appli
c	20	34.8	4.2	4152	3	US-09-712-813-5	Sequence 5, Appli
c	21	34.8	4.2	4152	3	US-09-700-354A-5	Sequence 5, Appli
c	22	34.8	4.2	5570	3	US-09-902-540-623	Sequence 623, App
c	23	34.6	4.2	2040	2	US-08-031-538-10	Sequence 10, Appl
c	24	34.4	4.1	1123	3	US-09-902-540-223	Sequence 223, App
	25	34.4	4.1	1123	3	US-09-902-540-6000	Sequence 6000, Ap
c	26	34.2	4.1	9408	3	US-09-949-016-13867	Sequence 13867, A
c	27	34.2	4.1	13187	3	US-09-422-936-61	Sequence 61, Appl
	28	34.2	4.1	127280	3	US-09-949-016-14857	Sequence 14857, A
	29	34.2	4.1	132266	3	US-09-949-016-14860	Sequence 14860, A
	30	34.2	4.1	150833	3	US-09-949-016-14859	Sequence 14859, A
	31	34.2	4.1	159963	3	US-09-949-016-14858	Sequence 14858, A
	32	34.2	4.1	171130	3	US-09-949-016-14861	Sequence 14861, A
c	33	34.2	4.1	784019	3	US-09-949-016-14033	Sequence 14033, A
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	37	33.8	4.1	601	3	US-09-949-016-45044	Sequence 45044, A
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	40	33.8	4.1	601	3	US-09-949-016-140296	Sequence 140296,
	41	33.8	4.1	601	3	US-09-949-016-140297	Sequence 140297,
c	42	33.8	4.1	601	3	US-09-949-016-142346	Sequence 142346,
c	43	33.8	4.1	601	3	US-09-949-016-142347	Sequence 142347,
c	44	33.8	4.1	1558	3	US-09-949-016-764	Sequence 764, App
c	45	33.8	4.1	1558	3	US-09-949-016-4025	Sequence 4025, Ap

ALIGNMENTS

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RESULT 1
US-09-902-540-908/c
; Sequence 908, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
;  APPLICANT: Goldman, Barry S.
;  APPLICANT: Hinkle, Gregory J.
;  APPLICANT: Slater, Steven C.
;  APPLICANT: Wiegand, Roger C.
;  TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
;  FILE REFERENCE: 38-1015849)B
;  CURRENT APPLICATION NUMBER: US/09/902,540
;  CURRENT FILING DATE: 2001-07-10
;  PRIOR APPLICATION NUMBER: 60/217,883
;  PRIOR FILING DATE: 2000-07-10
;  NUMBER OF SEQ ID NOS: 16825
;  SEQ ID NO 908
;  LENGTH: 9007
;  TYPE: DNA
;  ORGANISM: Myxococcus xanthus
US-09-902-540-908

Query Match          5.1%;  Score 42.4;  DB 3;  Length 9007;
Best Local Similarity   58.9%;  Pred. No. 0.058;
Matches   73;  Conservative    0;  Mismatches   51;  Indels    0;  Gaps    0;

Qy    330 TGGCCCCAGTCCCGGCCTCGGGCTTCCACCTTCCAGTCGCTGACCTGAACGATACAGGGG 389
              |||||| ||    ||  || ||||||||  ||||| || ||| || |||| || ||||
Db   7069 TGTCCACGGGGCCCCCGTCGTGCGGTCACCTGCCACCTGCTGACGCTGACCCCCACCGAACACGTGC 7010

Qy    390 AGTACTTCTGCATCTATCACACCTACCCTGATGGGACGTACACTGGGAGAATCTTCCTGG 449
              || |||| |||| |   ||||| |  ||  ||  |||| ||| || |||  || |||||
Db   7009 TGGTGCTGTGCATGCACCACCATCATCTCCGGACGGCTGGTCCATGGGCGTCGTCCGGG 6950

Qy    450 AGGT 453
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Db   6949 AAGT 6946

RESULT 2
US-09-621-976-17202
; Sequence 17202, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
;  APPLICANT: Dumas Milne Edwards, J.B.
;  APPLICANT: Jobert, S.
;  APPLICANT: Giordano, J.Y.
```

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Db      709 TCGGTGGCCGTCGCCGGCCGCCGACCTCAAGAGCGGCCAGACGATGATGAAGAGCGGTCATC 768
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RESULT 4
US-09-902-540-1257/c
; Sequence 1257, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
;  APPLICANT: Goldman, Barry S.
;  APPLICANT: Hinkle, Gregory J.
;  APPLICANT: Slater, Steven C.
;  APPLICANT: Wiegand, Roger C.
;  TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
;  FILE REFERENCE: 38-10(15849)B
;  CURRENT APPLICATION NUMBER: US/09/902,540
;  CURRENT FILING DATE: 2001-07-10
;  PRIOR APPLICATION NUMBER: 60/217,883
;  PRIOR FILING DATE: 2000-07-10
;  NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1257
;  LENGTH: 34316
;  TYPE: DNA
;  ORGANISM: Myxococcus xanthus
US-09-902-540-1257
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Best Local Similarity   47.1%;  Pred. No. 5.2;
Matches  113;  Conservative   0;  Mismatches  127;  Indels   0;  Gaps    0;

Qy      347 CTGGGCCTCACCCTCCAGTCGCTGACCGTGAACGATACAGGGGAGTACTTCTGCATCTAT 406
                |||    |      ||||    |||   |||||| |||| ||||||||| ||||||| ||||
Db    19370 CTGCCCGAGTCCTTCAAGAGCTGGGGAGAATCTTCCTGGAGGTCCTAGAAAGTCA 19311

Qy      407 CACACCTACCCTGATGGGACGTACACTGGGAGAATCTTCCTGGAGGTCCTAGAAAGTCA 466
                ||  ||       ||||         ||||
Db    19310 GACATCAACCCACCCACCGCGCTGTACACCTACCTACGGGCCCATCAAGGAGGGCGTGCCCTTCGCG 19251

Qy      467 GTGGCTGAGCACGGTGCCAGTTCCAGATTCCATTGCTTGGAGCCATGGCCGCGACGCTG 526
                |||||   |||   |     ||||   |      |||||||
Db    19250 AACGGCCCAACGCCAGCGTGGACACGCCCGGCCGTCCAGGAGGATGGGCCAAGCAGCAGGAG 19191

Qy      527 GTGGTCATCTGCACAGCAGTCATCGTGGTGCGCGTTGACTAGAAAGAAGAAAGCCCTC 586
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RESULT 5
US-09-154-750A-69
; Sequence 69, Application US/09154750A
; Patent No. 6432640
; GENERAL INFORMATION:
;  APPLICANT: Vogelstein, Bert
;  APPLICANT: Kinzler, Kenneth
;  APPLICANT: Polyak, Kornelia
;  TITLE OF INVENTION: p53-Induced Apoptosis
;  FILE REFERENCE: 1107.75357
;  CURRENT APPLICATION NUMBER: US/09/154,750A
;  CURRENT FILING DATE: 1998-09-17
;  PRIOR APPLICATION NUMBER: 60/059,153
;  PRIOR FILING DATE: 1997-09-17
;  PRIOR APPLICATION NUMBER: 60/079817
;  PRIOR FILING DATE: 1998-03-30
;  NUMBER OF SEQ ID NOS: 93
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 69
;  LENGTH: 993
;  TYPE: DNA
;  ORGANISM: Homo sapiens
US-09-154-750A-69
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;  TITLE OF INVENTION: ESTs and Encoded Human Proteins.
;  FILE REFERENCE: GENSET.054PR2
;  CURRENT APPLICATION NUMBER: US/09/621,976
;  CURRENT FILING DATE: 2000-07-21
;  NUMBER OF SEQ ID NOS: 19335
;  SOFTWARE: Patent.pm
; SEQ ID NO 17202
;  LENGTH: 364
;  TYPE: DNA
;  ORGANISM: Homo sapiens
US-09-621-976-17202
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Best Local Similarity   25.8%;  Pred. No. 0.27;
Matches   61;  Conservative  77;  Mismatches  77;  Indels   1;  Gaps    1;

Qy       47 CTGCTTCCTGTAGGCCCTCTGGGCAGAAGCATGCCGTGTCCTCCTCTGATCTGGGCC 106
               :::: ||   :| ||| ||| :  :| :::  |:| : : ||| |:|| :::||:::
Db      129 MWKYCYRKYRSRGMCCMWCAGSGMCYSRSAGSRYSKKGSRGRWTWKKGCSRATSKKGRWM 188

Qy      107 CAGGGGCTGAGGCAGGCTCCCCTCGCCTCAGGAATGATGACAGGCACAATAGAAACAACG 166
               :::.  :||| | |||| ||:::|   :| : :| :::: :::: ||: ::::
Db      189 WMKKGSRRRATSRYGMMSSMYGASKRMSSMCSASTRMSSASCMMYMMMSAGSYASCAWKM 248

Qy      167 GGGAACATTTCTGCAGAGAAAGGTGGCTCTATCATCTTACAATGTCACCTCTCCACC 226
               ::||::||:: :: ::| :| : :: :: :|: : |:
Db      249 SKYRRCAKWSCTYSWYMRASMKKSKYCAWSRKGSKCC-MYSRKGSKSCYCCWGGSCCCCG 307

Qy      227 ACGGCACAAGTGACCCAGGTCAACTGGGAGCAGCAGGACCAGCTTCTGCCATTTG 282
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RESULT 3
US-09-902-540-5256
; Sequence 5256, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
;  APPLICANT: Goldman, Barry S.
;  APPLICANT: Hinkle, Gregory J.
;  APPLICANT: Slater, Steven C.
;  APPLICANT: Wiegand, Roger C.
;  TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
;  FILE REFERENCE: 38-10(15849)B
;  CURRENT APPLICATION NUMBER: US/09/902,540
;  CURRENT FILING DATE: 2001-07-10
;  PRIOR APPLICATION NUMBER: 60/217,883
;  PRIOR FILING DATE: 2000-07-10
;  NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 5256
;  LENGTH: 1335
;  TYPE: DNA
;  ORGANISM: Myxococcus xanthus
US-09-902-540-5256
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Qy      347 CTGGGCCTCACCCTCCAGTCGCTGACCGTGAACGATACAGGGGAGTACTTCTGCATCTAT 406
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Db      529 CTGCCCGAGTCCTTCAAGAGCTGGGGAGAATCTTCCTGGAGGTCCTAGAAAGTCA 588

Qy      407 CACACCTACCCTGATGGGACGTACACTGGGAGAATCTTCCTGGAGGTCCTAGAAAGTCA 466
                |||  ||       ||||         ||||
Db      589 GACATCAACCCACCCACCGCGCTGTACACCTACCTACGGGCCCATCAAGGAGGGCGTGCCCTTCGCG 648

Qy      467 GTGGCTGAGCACGGTGCCAGTTCCAGATTCCATTGCTTGGAGCCATGGCCGCGACGCTG 526
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Db      649 AACGGCCCAACGCCAGCGTGGACACGCCCGGCCGTCCAGGAGGATGGGCCAAGCAGCAGGAG 708

Qy      527 GTGGTCATCTGCACAGCAGTCATCGTGGTGCGCGTTGACTAGAAAGAAGAAAGCCCTC 586
                |||  |||       |       |       ||||
Db      586
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            GenCore version 5.1.7
      Copyright (c) 1993 - 2006  Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on:   March  5, 2006, 20:46:53 ; Search time 4262 Seconds
                                   (without alignments)
                                   11083.273 Million cell updates/sec

Title:        US-10-658-482-1
Perfect score:  831
Sequence:     1 cgtcctactcgagtcggct........caaccagaggcatcttctgg 831

Scoring table:  IDENTITY.NUC
                Gapop 10.0 , Gapext 1.0

Searched:     583141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters:     11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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              4: gb_om:*
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             11: gb_sy:*
             12: gb_un:*
             13: gb_vi:*
             14: gb_htg:*
             15: gb_pl:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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3	788	94.8	1448	8	BC101289	BC101289 Homo sapi
4	788	94.8	1452	8	BC101291	BC101291 Homo sapi
5	786.4	94.8	1448	8	BC101288	BC101288 Homo sapi
6	785.8	94.6	2139	6	AX834616	AX834616 Sequence
7	785.8	94.6	2139	8	AK097192	AK097192 Homo sapi
8	670	80.6	2893	8	HSM807055	BX640915 Homo sapi
9	344	41.4	344	6	CQ717323	CQ717323 Sequence
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c 11	333.6	40.1	144213	14	AC073407	AC073407 Homo sapi
12	333.6	40.1	151535	14	AC084188	AC084188 Homo sapi
13	333.6	40.1	161077	8	AC093010	AC093010 Homo sapi
c 14	333.6	40.1	181988	14	AC090552	AC090552 Homo sapi
c 15	333.6	40.1	196832	14	AC027054	AC027054 Homo sapi
c 16	333.6	40.1	318586	14	AC107422	AC107422 Homo sapi
17	282	33.9	297	6	AX119215	AX119215 Sequence
18	259	31.2	131161	14	AC068938	AC068938 Homo sapi
19	259	31.2	318586	14	AC107422	AC107422 Homo sapi
20	234.6	28.2	220524	14	AC103065	AC103065 Rattus no
21	234.6	28.2	248938	14	AC095006	AC095006 Rattus no
22	234.6	28.2	253874	14	AC131560	AC131560 Rattus no
c 23	234.6	28.2	253874	14	AC110414	AC110414 Rattus no
c 24	233.6	28.1	158312	9	AC154408	AC154408 Mus muscu
25	184.6	22.2	70384	14	AC103977	AC103977 Homo sapi
26	149.2	18.0	157	6	CQ454533	CQ454533 Sequence
c 27	139.8	16.8	151535	14	AC084188	AC084188 Homo sapi
28	128	15.4	218995	9	AC120871	AC120871 Mus muscu
29	79	9.5	294	10	AB143947	AB143947 Homo sapi
30	77.2	9.3	207095	14	AC136844	AC136844 Rattus no
c 31	45.4	5.5	125020	8	AF429315	AF429315 Homo sapi
c 32	43	5.2	125020	8	AF429315	AF429315 Homo sapi
33	42.4	5.1	9007	6	AR619513	AR619513 Sequence
c 34	40.6	4.9	30242	1	AE016790	AE016790 Pseudomon
c 35	40.2	4.8	177661	9	AC119237	AC119237 Mus muscu
c 36	40.2	4.8	195768	8	AC022034	AC022034 Homo sapi
c 37	40.2	4.8	20574	14	AC162176	AC162176 Mus muscu
38	40	4.8	2000	7	AX655393	AX655393 Sequence
c 39	39.8	4.8	205893	14	AC115530	AC115530 Rattus no
c 40	39.8	4.8	293757	9	AC095491	AC095491 Rattus no
41	39.6	4.8	410	7	X69545	X69545 H.sapiens g
c 42	39.4	4.7	169989	8	AC090137	AC090137 Homo sapi
43	39.4	4.7	174345	14	AC025236	AC025236 Homo sapi
c 44	39.4	4.7	174646	14	AC087355	AC087355 Homo sapi
c 45	39.4	4.7	181727	14	AC036232	AC036232 Homo sapi

ALIGNMENTS

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RESULT 1
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LOCUS       BD260690              1332 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  50 human secreted proteins.
ACCESSION   BD260690
VERSION     BD260690.1  GI:33070460
KEYWORDS    JP 2002539814-A/32.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1332)
AUTHORS     Rosen,C.A., Ruben,S.M. and Komatsoulis,G.
TITLE       50 human secreted proteins
JOURNAL     Patent: JP 2002539814-A 32 26-NOV-2002;
            HUMAN GENOME SCIENCES INC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002539814-A/32
            PD   26-NOV-2002
            PF   22-MAR-2000 JP 2000608034
            PR   26-MAR-1999 US   60/126594,17-DEC-1999 US    60/172408 PI
            CRAIG A ROSEN,STEVEN M RUBEN,GEORGE KOMATSOULIS PC
            C12N15/09,A61K38/00,A61K48/00,A61P1/00,A61P1/04,A61P3/10 PC
            ,A61P7/02,A61P7/04,
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            PC   C12N1/15,
            PC   C12N1/19,C12N1/21,C12N5/10,C12P21/02,C12Q1/02,C12Q1/68,G01N33/
            PC   53,
            PC   G01N33/566,G01N33/68,C12N15/00,A61K37/02,C12N5/00 CC    50
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                          /db_xref="taxon:9606"

Query Match       98.5%;  Score 818.4;  DB 6;  Length 1332;
Best Local Similarity   99.8%;  Pred. No. 2.6e-214;
Matches   830;  Conservative   0;  Mismatches   1;  Indels   1;  Gaps   1;

Qy      1  CGTCCTATCTGCAGTCGGCTACTTTCAGT-GGCAGAAGAGGCCACATCTGCTTCCTGTAG   59
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Db    235  CGTCCTATCTGCAGTCGGCTACTTTCAGTGGGCAGAAGAGGCCACATCTGCTTCCTGTAG  294

Qy     60  GCCCTCTGGGCAGAAGCATGCGCTGGTGTCTCCTCCTGATCTGGGCCCAGGGGCTGAGGC  119
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    295  GCCCTCTGGGCAGAAGCATGCGCTGGTGTCTCCTCCTGATCTGGGCCCAGGGGCTGAGGC  354

Qy    120  AGGCTCCCCTCGCCTCAGGAATGATGACAGGCACAATAGAAACAACGGGGAACATTTCTG  179
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Qy    480  GTGCCAGGTTCCAGATTCCATTGCTTGGAGCCATGGCCGCGACGCTGGTGGTCATCTGCA  539
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Qy    600  TGGAAGGTGACCTCAGGAGAAAATCAGTCTGGACAGGAGGAATGGAGCCCCAGTGCTCCCT  659
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Qy    720  GGGGAGGAGGACTGTGCCGAGCTGCGAGCTGCACTACTTCAAGTGCTCCTGAGTTACAGAAGCCTGG  779
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LOCUS       BC101290               1446 bp    mRNA    linear    PRI 02-AUG-2005
DEFINITION  Homo sapiens hypothetical protein FLJ39873, mRNA (cDNA clone
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ACCESSION   BC101290
VERSION     BC101290.1  GI:71680560
KEYWORDS    MGC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1446)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
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            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
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            Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
            Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
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            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  CONSRTM   Mammalian Gene Collection Program Team
  TITLE     Generation and initial analysis of more than 15,000 full-length
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  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   PUBMED   12477932
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  CONSRTM   NIH MGC Project
  TITLE     Direct Submission
  JOURNAL   Submitted (01-AUG-2005) National Institutes of Health, Mammalian
            Gene Collection (MGC), Bethesda, MD 20892-2590, USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Baylor Human Genome Sequencing Center
            cDNA Library Preparation: Baylor Human Genome Sequencing Center
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Sequencing Group at the Stanford Human Genome
            Center, Stanford University School of Medicine, Stanford, CA 94305
            Web site:         http://www.shgc.stanford.edu
            Contact:  (Dickson, Mark) mcd@paxil.stanford.edu
            Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
            R. M.
            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
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     Copyright (c) 1993 - 2006  Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched:   4996997 seqs, 333234608 residues

Total number of hits satisfying chosen parameters:    9993994

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
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	2	831	100.0	1711	9	ADA21190	Ada21190 Human sec
	3	818.4	98.5	1332	3	AAC95484	Aac95484 Human sec
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	5	796	95.8	860	10	ADF76824	Adf76824 Novel hum
	6	785.8	94.6	2139	11	ADM03055	Adm03055 Human cDN
	7	775.8	93.4	1500	10	ADE07073	Ade07073 Novel cod
	8	775.8	93.4	1500	14	ADU40230	Adu40230 Novel hum
	9	696.8	83.9	1164	10	ADE08854	Ade08854 Novel DNA
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	14	40.6	4.9	1590	8	ACA43911	Aca43911 Prokaryot
c	15	40	4.8	2000	8	ADA71938	Ada71938 Rice gene
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	17	36.8	4.4	1335	14	ACL68793	Acl68793 M. xanthu
	18	36.8	4.4	34316	14	ACL64794	Acl64794 M. xanthu
c	19	36	4.3	993	2	AAX86266	Aax86266 DNA encod
	20	36	4.3	993	6	ABL68586	Abl68586 Kidney ca
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	41	35	4.2	2000	6	ABQ60910	Abq60910 Clone IMA
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	44	35	4.2	2662	8	ABX70867	Abx70867 Novel hum
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ALIGNMENTS

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AC   ADM32155;
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DT   17-JUN-2004  (first entry)
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DE   PRO52254 cDNA, seq id 1.
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KW   Immunosuppressive; dermatological; hepatotropic; nephrotropic;
KW   antidiabetic; antiasthmatic; antipsoriatic; antiallergic; antianaemic;
KW   antiarteriosclerotic; antiarthritic; neuroprotective; respiratory;
KW   antiinflammatory; gene therapy; rheumatoid arthritis; asthma; gene; ss.
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PN   WO2004024068-A2.
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PD   25-MAR-2004.
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PF   09-SEP-2003; 2003WO-US028202.
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PR   11-SEP-2002; 2002US-0410062P.
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PA   (GETH ) GENENTECH INC.
XX
PI   Baldwin DT,  Bodary SC,  Chan AC,  Clark H,  Jackman JK,  Wood WI;
XX
DR   WPI; 2004-269871/25.
DR   P-PSDB; ADM32156.
XX
PT   New PRO52254 nucleic acid or polypeptide, useful for preparing a
PT   composition for diagnosing or treating in a mammal an immune related
PT   disorder e.g. systemic lupus erythematosus.
XX
PS   Claim 3; SEQ ID NO 1; 100pp; English.
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XX
CC   The invention relates to an isolated PRO52254 nucleic acid. Further
CC   disclosed is a vector comprising the nucleic acid. The PRO52254 nucleic
CC   acid or polypeptide is useful for preparing a composition for diagnosing
CC   or treating an immune related disorder, e.g., systemic lupus
CC   erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic
CC   arthritis, spondyloarthropathy, systemic sclerosis, idiopathic
CC   inflammatory myopathy, Sjogren's syndrome, systemic vasculitis,
CC   sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopaenia,
CC   thyroiditis, diabetes mellitus, immune-mediated renal disease, a
CC   demyelinating disease of the central or peripheral nervous system,
CC   idiopathic demyelinating polyneuropathy, Guillain-Barr syndrome, chronic
CC   inflammatory demyelinating polyneuropathy, hepatobiliary disease,
CC   infectious or autoimmune chronic active hepatitis, primary biliary
CC   cirrhosis, granulomatous hepatitis, sclerosing cholangitis, inflammatory
CC   bowel disease, gluten-sensitive enteropathy, Whipple's disease,
CC   autoimmune or immune-mediated skin disease, bullous skin disease,
CC   erythema multiforme, contact dermatitis, psoriasis, allergic disease,
CC   asthma, allergic rhinitis, atopic dermatitis, food hypersensitivity,
CC   urticaria, immunologic disease of the lung, eosinophilic pneumonias,
CC   idiopathic pulmonary fibrosis, hypersensitivity pneumonias,
CC   transplantation associated disease, graft rejection or graft-versus-host-
CC   disease. The current sequence represents the PRO52245 nucleotide
CC   sequence.
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ID   ADA21190 standard; cDNA; 1711 BP.
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AC   ADA21190;
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DT   20-NOV-2003 (first entry)
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KW   antiarteriosclerotic; antiasthmatic; immunosuppressive; antithyroid;
KW   cytostatic; hepatotropic; dermatological; antidiabetic; nephrotropic;
KW   antigout; thyromimetic; neuroprotective; osteopathic; antiarthritic;
KW   antiparasitic; antihelminthic; antipsoriatic; uropathic;
KW   ophthalmological; antirheumatic; haemostatic; antibacterial; virucide;
KW   protozoacide; fungicide; gene therapy; cell proliferative disorder;
KW   arteriosclerosis; atherosclerosis; cirrhosis; hepatitis;
KW   paroxysmal nocturnal haemoglobinuria; polycythaemia vera; psoriasis;
KW   primary thrombocytopaenia; cancer; developmental disorder;
KW   renal tubular acidosis; anaemia; mental retardation;
KW   neurological disorder; Alzheimer's disease; Parkinson's disease;
KW   epilepsy; autoimmune disorder; inflammatory disorder; AIDS; allergy;
KW   asthma; autoimmune thyroiditis; glomerulonephritis; contact dermatitis; Crohn's disease;
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KW   Graves' disease; Hashimoto's thyroiditis; irritable bowel syndrome;
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PR   19-MAR-2002; 2002US-0366041P.
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PI   Khare R, Lee S, Lee SY, Richardson TW, Chang H;
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DR   WPI; 2003-689669/65.
DR   P-PSDB; ADA21139.
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PT   New human secreted proteins and polynucleotides, useful for diagnosing,
PT   treating or preventing autoimmune or inflammatory disorders (e.g. AIDS,
PT   allergy, asthma or anemia), multiple sclerosis, osteoporosis, cancer or
PT   hepatitis.

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                    GenCore version 5.1:7
          Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on:    March  5, 2006, 20:49:07 ; Search time 3728 Seconds
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            8: gb_est7:*
            9: gb_gss1:*
           10: gb_gss2:*
           11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
```

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	831	100.0	3809	4	HSM804486	AL833175 Homo sapi
	2	763	91.8	763	11	DQ045305	DQ045305 Homo sapi
	3	666.4	80.2	693	5	BX089912	BX089912 BX089912
c	4	376	45.2	587	1	AA527161	AA527161 ni07c12.8
	5	367.6	44.2	558	8	DN401602	DN401602 LIB4004-0
c	6	363	43.7	508	2	AA527065	AA527065 ni06g12.8
·	7	343.6	41.3	627	5	BX914278	BX914278 BX914278
c	8	308.2	37.1	314	8	DN995825	DN995825 TC124474
c	9	256.4	30.9	402	7	AA505489	AA505489 nh96c03.s
c	10	229	27.6	526	2	BG211784	BG211784 RST31353
c	11	167.4	20.1	530	2	BF875718	BF875718 QV3-ET010
c	12	148.2	17.8	251	1	AA353061	AA353061 EST61135
c	13	138.4	16.7	272	7	CV307751	CV307751 tj46f07.b
	14	138.4	16.7	272	7	CV307752	CV307752 tj46f07.g
c	15	136.6	16.4	243	7	CV307662	CV307662 tj46a07.b
c	16	136.6	16.4	243	7	CV307663	CV307663 tj46a07.g
c	17	136	16.4	241	7	CV307731	CV307731 tj46e07.b
c	18	136	16.4	241	7	CV307732	CV307732 tj46e07.g
c	19	135.6	16.3	239	7	CV305235	CV305235 ti40g07.b
c	20	135.6	16.3	239	7	CV305236	CV305236 ti40g07.g
	21	135.6	16.3	239	7	CV307711	CV307711 tj46d07.b
c	22	135.6	16.3	239	7	CV307712	CV307712 tj46d07.g
	23	135.6	16.3	239	7	CV307772	CV307772 tj46g07.b
c	24	135.6	16.3	239	7	CV307773	CV307773 tj46g07.g
	25	131	15.8	315	7	CN446831	CN446831 tj46b07.5
c	26	131	15.8	315	7	CV307678	CV307678 tj46b07.b
c	27	116	14.0	263	4	AW512550	AW512550 xx64d09.x
c	28	102.4	12.3	238	3	BQ333892	BQ333892 QV3-ET010
	29	100.6	12.1	275	5	BQ377877	BQ377877 QV1-UM003
	30	94.4	11.1	94	11	DQ045306	DQ045306 Pan trogl
	31	80.8	9.7	519	9	AQ248174	AQ248174 HS_2045_B
	32	76.4	9.2	511	10	CE708684	CE708684 tigr-gss-
c	33	76.4	9.2	680	9	CE116328	CE116328 tigr-gss-
c	34	64.8	7.8	658	9	BZ224666	BZ224666 CH230-496
c	35	54	6.5	585	2	BI055269	BI055269 PM0-GN034
	36	42.6	5.1	602	6	CA727769	CA727769 wdi1c.pk0
	37	40.8	4.9	658	6	CA497669	CA497669 WHE3230_G
	38	40.4	4.9	226	6	CF250573	CF250573 esa014_d0
c	39	40.2	4.8	936	6	CB953913	CB953913 AGENCOURT
	40	39.6	4.8	790	2	BF537732	BF537732 60205442 6
	41	39.4	4.7	565	10	CNS02J5A	AL199783 Tetraodon
	42	39.4	4.7	629	6	CA596296	CA596296 wpa1c.pk0
c	43	39.4	4.7	1780	4	CNS0GOT3	CR728177 Tetraodon
	44	39.2	4.7	1145	6	CD506105	CD506105 CDA77-D07
c	45	39.2	4.7	1379	2	BG396489	BG396489 60245921 7

ALIGNMENTS

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RESULT 1
HSM804486
LOCUS       HSM804486              3809 bp    mRNA    linear   HTC 16-APR-2005
DEFINITION  Homo sapiens mRNA; cDNA DKFZp667A205 (from clone DKFZp667A205).
ACCESSION   AL833175
VERSION     AL833175.1  GI:21733802
KEYWORDS    HTC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 3809)
  AUTHORS   Bloecker,H., Boecher,M., Brandt,P., Mewes,H.W., Weil,B., Amid,C.,
            Osanger,A., Fobo,G., Han,M. and Wiemann,S.
  CONSRTM   The German cDNA Consortium
  TITLE     Direct Submission
  JOURNAL   Submitted (20-JAN-2005) MIPS, Ingolstaedter Landstr-1, D-85764
            Neuherberg, GERMANY
COMMENT     Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
            sequenced by GBF (National Research Centre for Biotechnology Ltd.,
            Braunschweig/Germany) within the cDNA sequencing consortium of the
            German Genome Project.
            This clone (DKFZp667A205) is available at the RZPD Deutsches
            Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany.
            Please contact RZPD for ordering:
            http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp667A205
            Further information about the clone and the sequencing project is
            available at http://mips.gsf.de/projects/cdna/.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
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                     DH10B; sites NotI + SalI"
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                    /translation="MAFIVAHFMQFVILITTLCVFNMVFAKLGFSETVFSQRLSFTVL
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                    TLQSLTVNDTGEYFCIYHTYPDGTYTGRIFLEVLESSVAEHGARFQIPLLGAMAATLV
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ORIGIN

Query Match       100.0%;     Score 831;    DB 4;   Length 3809;
Best Local Similarity   100.0%;     Pred. No. 2.8e-221;
Matches  831;    Conservative   0;    Mismatches   0;    Indels   0;    Gaps   0;

Qy       1  CGTCCTATCTGCAGTCGGCTACTTTCAGTGGCAGAAGAGGCCACATCTGCTTCCTGTAGG     60
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Db    2741  CGTCCTATCTGCAGTCGGCTACTTTCAGTGGCAGAAGAGGCCACATCTGCTTCCTGTAGG  2800

Qy      61  CCCTCTGGGGCAGAAGCATGCGCTGTGTCTTCCTCCTGATCTGGGCCCAGGGGCTGAGGCA    120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2801  CCCTCTGGGGCAGAAGCATGCGCTGTGTCTTCCTCCTGATCTGGGCCCAGGGGCTGAGGCA  2860

Qy     121  GGCTCCCCCTCGCCTCAGGAATGATGACAGGCACAATAGAAACAACGGGAACAATTTCTGC    180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2861  GGCTCCCCCTCGCCTCAGGAATGATGACAGGCACAATAGAAACAACGGGAACAATTTCTGC  2920

Qy     181  AGAGAAAGGTGGCTCTATCATCTTACAATGTCACCTCTCCACCACGGCACAAGTGAC    240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2921  AGAGAAAGGTGGCTCTATCATCTTACAATGTCACCTCTCCACCACGGCACAAGTGAC  2980

Qy     241  CCAGGTCAACTGGGAGCAGCAGGACCAGCTTCTGGCCATTGTAATGCTGACTTGGGGTG    300
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Db    2981  CCAGGTCAACTGGGAGCAGCAGGACCAGCTTCTGGCCATTGTAATGCTGACTTGGGGTG  3040

Qy     301  GCACATCTCCCATCCTTCAAGGATCGAGTGGCCCCAGGTGCCGGCCTGGCCTTCACCCT    360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3041  GCACATCTCCCATCCTTCAAGGATCGAGTGGCCCCAGGTGCCGGCCTGGGCCTTCACCCT  3100

Qy     361  CCAGTCGCTGCTGACCGTGAACGATACAGGGGAGTACTTCTGCATCTATCACACACTACCCTGA    420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3101  CCAGTCGCTGCTGACCGTGAACGATACAGGGGAGTACTTCTGCATCTATCACACACTACCCTGA  3160

Qy     421  TGGGACGTACACTGGGAGAATCTTCCTGGAGGTCCTAGAAAGTCCAGTGGCTGACGCACGG    480
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3161  TGGGACGTACACTGGGAGAATCTTCCTGGAGGTCCTAGAAAGTCCAGTGGCTGACGCACGG  3220

Qy     481  TGCCAGGTTCCAGATTCCATTGCTTGGAGCCATGGCCGCGACGCGTGGTGTCATCTGCAC    540
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3221  TGCCAGGTTCCAGATTCCATTGCTTGGAGCCATGGCCGCGACGCGTGGTGTCATCTGCAC  3280

Qy     541  AGCAGTCATCGTGGTGCCGGTTGACTAGAAAGAAGAAGAAAGCCCTCAGAATCCATTCTGT    600
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3281  AGCAGTCATCGTGGTGCCGGTTGACTAGAAAGAAGAAGAAAGCCCTCAGAATCCATTCTGT  3340

Qy     601  GGAAGGTGACCTCAGGAGAAAATCAGCTGACAGGAGGAATGGAGCCCCAGTGCTCCCTC    660
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3341  GGAAGGTGACCTCAGGAGAAAATCAGCTGACAGGAGGAATGGAGCCCCAGTGCTCCCTC  3400

Qy     661  ACCCCCAGGAAGCTGTGTCCAGGCAGAAGCTGCACCTGCTCTGGGCTTCGTCTGGAGAGCAGCG    720
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Db    3401  ACCCCCAGGAAGCTGTGTCCAGGCAGAAGCTGCACCTGCTCTGGGCTTCGTCTGGAGAGCAGCG  3460

Qy     721  GGGAGGAGGACTGTGCCGAGCTGCACTGACTACTTCAATGTCCTGAGTTACAGAAGCCTGGG    780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3461  GGGAGGAGGACTGTGCCGAGCTGCATGACTACTTCAATGTCCTGAGTTACAGAAGCCTGGG  3520

Qy     781  TAACTGCAGCTTCTTCACAGAGACTGGTTAGCAACCAGAGGCATCTTCTGG  831
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Db    3521  TAACTGCAGCTTCTTCACAGAGACTGGTTAGCAACCAGAGGCATCTTCTGG  3571
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RESULT 2
DQ045305
LOCUS        DQ045305              763 bp    DNA    linear    GSS 02-JUN-2005
DEFINITION   Homo sapiens HC11059 gene, VIRTUAL TRANSCRIPT, partial sequence,
             genomic survey sequence.
ACCESSION    DQ045305
VERSION      DQ045305.1  GI:66896520
KEYWORDS     GSS.
SOURCE       Homo sapiens (human)
  ORGANISM   Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
             Hominidae; Homo.
REFERENCE    1 (bases 1 to 763)
  AUTHORS    Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
             Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,
             White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
  TITLE      A Scan for Positively Selected Genes in the Genomes of Humans and
             Chimpanzees
  JOURNAL    (er) PLoS Biol. 3 (6), E170 (2005)
   PUBMED    15869325
REFERENCE    2 (bases 1 to 763)
  AUTHORS    Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
             Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,
             White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
  TITLE      Direct Submission
  JOURNAL    Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
             Rockville, MD 20850, USA
COMMENT      This sequence was made by sequencing genomic exons and ordering
             them based on alignment. Translation starts at the beginning of
             alignment.
FEATURES             Location/Qualifiers
     source          1..763
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
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ORIGIN

Query Match       91.8%;     Score 763;    DB 11;    Length 763;
Best Local Similarity   100.0%;     Pred. No. 2e-202;
Matches  763;    Conservative   0;    Mismatches   0;    Indels   0;    Gaps   0;

Qy      44  CATCTGCTTCCTGTAGGCCCTCTGGGCAGAAGCATGCGCTGGTGTCTTCCTCCTGATCTGG    103
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Db       1  CATCTGCTTCCTGTAGGCCCTCTGGGCAGAAGCATGCGCTGGTGTCTTCCTCCTGATCTGG     60

Qy     104  GCCCAGGGGCTGAGGCAGGCAGGCTCCCCTCGCCTCAGGAATGATGACAGGCACAATAGAAACA    163
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61  GCCCAGGGGCTGAGGCAGGCAGGCTCCCCTCGCCTCAGGAATGATGACAGGCACAATAGAAACA    120

Qy     164  ACGGGAACAATTTCTGCAGAGAAAGGTGGCTCTATCATCTTACAATGTCACCTCTCCTCC    223
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121  ACGGGAACAATTTCTGCAGAGAAAGGTGGCTCTATCATCTTACAATGTCACCTCTCCTCC    180

Qy     224  ACCACGGCACAAGTGACCAAGTCAACTGGGAGCAGCAGGACCAGCTTCTGGCCATTTGT    283
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181  ACCACGGCACAAGTGACCAAGTCAACTGGGAGCAGCAGGACCAGCTTCTGGCCATTTGT    240

Qy     284  AATGCTGACTTGGGGTGGCACATCTGGGGTTCAAGGATGGCCCCCAGGTCCC    343
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241  AATGCTGACTTGGGGTGGCACATCTGGGGTTCAAGGATGGCCCCCAGGTCCC    300

Qy     344  GGCCTGGCCTCACCCTCCAGTCGCTGACCGTGAACGATACAGGGGAGTACTTCTGCATC    403
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Db     301  GGCCTGGCCTCACCCTCCAGTCGCTGACCGTGAACGATACAGGGGAGTACTTCTGCATC    360
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GenCore version 5.1.7
Copyright (c) 1993 - 2006   Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 5, 2006, 20:55:02 ; Search time 827 Seconds
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                                           8309.375 Million cell updates/sec

Title: US-10-658-482-1
Perfect score: 831
Sequence: 1 cgtcctatctgcagtcggct.........caaccagaggcatcttctgg 831

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published_Applications_NA_Main:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	796	95.8	860	8	US-10-370-715B-499	Sequence 499, App
2	785.8	94.6	2139	6	US-10-108-260A-1740	Sequence 1740, Ap
3	775.8	93.4	1500	9	US-10-128-558-15	Sequence 15, Appl
4	376	45.2	587	9	US-10-756-149-1939	Sequence 1939, Ap
c 5	203.4	24.5	247	3	US-09-796-692-9142	Sequence 9142, Ap
c 6	203.4	24.5	247	5	US-10-040-862-9142	Sequence 9142, Ap
c 7	203.4	24.5	247	6	US-10-057-475B-9142	Sequence 9142, Ap
c 8	203.4	24.5	247	6	US-10-154-884B-9142	Sequence 9142, Ap
c 9	203.4	24.5	247	6	US-10-764-324-9142	Sequence 9142, Ap
10	79	9.5	294	8	US-10-674-124A-5607	Sequence 5607, Ap
11	40.6	4.9	1590	7	US-10-282-122A-31781	Sequence 31781, A
12	36.8	4.4	693	5	US-10-123-155-406	Sequence 406, App
13	36.8	4.4	693	6	US-10-146-731-406	Sequence 406, App
14	36.8	4.4	693	6	US-10-140-472-406	Sequence 406, App
15	36.8	4.4	693	6	US-10-141-761-406	Sequence 406, App
16	36.8	4.4	693	6	US-10-142-885-406	Sequence 406, App
17	36.8	4.4	693	6	US-10-158-790-406	Sequence 406, App
18	36.8	4.4	693	6	US-10-137-871-406	Sequence 406, App
19	36.8	4.4	693	6	US-10-140-923-406	Sequence 406, App
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22	36.8	4.4	693	6	US-10-140-805-406	Sequence 406, App
23	36.8	4.4	693	6	US-10-140-864-406	Sequence 406, App
24	36	4.3	993	3	US-09-154-750A-69	Sequence 69, Appl
25	36	4.3	993	3	US-09-880-107-3943	Sequence 3943, Ap
26	36	4.3	993	3	US-09-968-007A-453	Sequence 453, Appl
27	36	4.3	993	8	US-10-802-432-28	Sequence 28, Appl
28	36	4.3	993	9	US-10-723-860-1071	Sequence 1071, Ap
29	36	4.3	993	9	US-10-843-641A-6923	Sequence 6923, Ap
30	36	4.3	1049	5	US-10-123-155-358	Sequence 358, App
c 31	36	4.3	1049	6	US-10-146-731-358	Sequence 358, App
c 32	36	4.3	1049	6	US-10-140-472-358	Sequence 358, App
c 33	36	4.3	1049	6	US-10-141-761-358	Sequence 358, App
c 34	36	4.3	1049	6	US-10-142-885-358	Sequence 358, App
c 35	36	4.3	1049	6	US-10-158-790-358	Sequence 358, App
c 36	36	4.3	1049	6	US-10-137-871-358	Sequence 358, App
37	36	4.3	1049	6	US-10-140-923-358	Sequence 358, App
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41	36	4.3	1049	6	US-10-140-864-358	Sequence 358, App
42	35.8	4.3	26729	6	US-10-283-247-6	Sequence 6, Appli
43	35.8	4.3	26729	10	US-11-143-787-6	Sequence 6, Appli
44	35.8	4.3	70383	6	US-11-283-247-3	Sequence 3, Appli
45	35.8	4.3	70383	10	US-11-143-787-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-10-370-715B-499

; Sequence 499, Application US/10370715B
; Publication No. US20040258678A1
; GENERAL INFORMATION:
; Patin Docket Preview
; APPLICANT: BODARY, SARAH C.
; APPLICANT: CLARK, HILLARY
; APPLICANT: BRISDELL, HUNTE
; APPLICANT: JACKMAN, JANET
; APPLICANT: SCHOENFELD, JILL R.
; APPLICANT: WILLIAMS, P. MICKEY
; APPLICANT: WOOD, WILLIAM I.
; APPLICANT: WU, THOMAS D.
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Immune
; TITLE OF INVENTION: Related Diseases
; FILE REFERENCE: P1948R1-US
; CURRENT APPLICATION NUMBER: US/10/370,715B
; CURRENT FILING DATE: 2003-02-21
; NUMBER OF SEQ ID NOS: 742
; SEQ ID NO 499
; LENGTH: 860
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-370-715B-499

Query Match   95.8%; Score 796; DB 8; Length 860;
Best Local Similarity   100.0%; Pred. No. 6.2e-252;
Matches 796; Mismatches   0; Conservative   0; Indels   0; Gaps   0;

Qy   36 AGAGGCCACATCTGCTTCCTGTAGGCCCTCTGGGCAGAAGCATGCGGCTGGTGTCTCCTCC 95
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Db   1 AGAGGCCACATCTGCTTCCTGTAGGCCCTCTGGGCAGAAGCATGCGGCTGGTGTCTCCTCC 60

Qy   96 TGATCTGGGCCCAGGGCTGAGGCAGGCTCCCTGCCTCAGGAATGATGACAGGCACAA 155
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Db   61 TGATCTGGGCCCAGGGCTGAGGCAGGCTCCCTGCCTCAGGAATGATGACAGGCACAA 120

Qy   156 TAGAAACAACGGGAACATTTCTGCAGAGAAAGGTGGCTCTATCATCTTACAAATGTCACC 215
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Qy   463 CTCAGTGGCTGAGCACGTGCCAGGTTCCAGATTCCATTGCTTGGGAGCCATTGGCCGCGAC 522
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Qy   823 ATCTTCTGG 831
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Qy   336 CAGTCCCGGCCTCCGGCCTGGCCTCACCCTCCAGTCGCTGACCGTGACCGTGACCGTGACGATACAGGGGAGTACT 395
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Qy   456 TAGAAAGCTCAGTGGCTGAGCACGTGCCAGGTTCCAGATTCCATTGCTTGGAGCCATGG 515
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Qy   756 ATGTCCTGAGTTACAGAAGCCTGGGTAACTGCAGCTTCTTCACAGAGACTGGTTAGCAAC 815
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Db   721 ATGTCCTGAGTTACAGAAGCCTGGGTAACTGCAGCTTCTTCACAGAGACTGGTTAGCAAC 780

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Query Match   94.6%; Score 785.8; DB 6; Length 2139;
Best Local Similarity   99.7%; Pred. No. 1.9e-248;
Matches   787; Conservative   0; Mismatches   2; Indels   0; Gaps   0;

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Qy   103 GGCCCAGGGGCTGAGGCAGGCTCCCCTGCCTCAGGAATGATGACAGGCACAATAGAAAC 162
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Qy   163 AACGGGGAACATTTCTGCAGAGAAAGGTGGCTCTATCATCTTACAATGTCACCTCCTC 222
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                GenCore version 5.1.7
        Copyright (c) 1993 - 2006 Biocceleration Ltd.

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Searched:       7218535 seqs, 109624Z582 residues

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Minimum DB seq length: 0
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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c	1	35.6	4.3	340000	12	US-11-102-978-3		Sequence 3, Appli
c	2	34.8	4.2	1285	8	US-10-750-185-54718		Sequence 54718, A
c	3	34.8	4.2	1285	8	US-10-750-623-54718		Sequence 54718, A
c	4	34.8	4.2	1694	8	US-10-689-742-49		Sequence 49, Appl
c	5	34.8	4.2	3187	8	US-10-947-249-189		Sequence 189, App
c	6	34.6	4.1	142605	12	US-11-121-086-64		Sequence 64, Appl
c	7	34.2	4.1	1125000	8	US-10-995-561-13286		Sequence 13286, A
c	8	34	4.1	801	6	US-09-925-065A-63566		Sequence 63566, A
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c	12	33.6	4.0	37507	8	US-10-522-037-2		Sequence 2, Appli
c	13	33.4	4.0	44617	7	US-10-330-773-928		Sequence 928, App
	14	33.2	4.0	201	8	US-10-995-561-9475		Sequence 9475, Ap
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	20	33.2	4.0	2333	8	US-10-995-561-343		Sequence 343, App
	21	33.2	4.0	2553	8	US-10-995-561-344		Sequence 344, App
	22	33.2	4.0	2748	8	US-10-995-561-348		Sequence 348, App
	23	33.2	4.0	3287	8	US-10-995-561-346		Sequence 346, App
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c	35	32.8	3.9	2663	12	US-11-000-463-693		Sequence 693, App
	36	32.8	3.9	34680	12	US-09-925-065A-265902		Sequence 265902,
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	38	32.4	3.9	1492	8	US-10-750-185-26396		Sequence 26396, A
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	40	32.4	3.9	1755	8	US-10-750-185-43052		Sequence 43052, A
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	42	32.4	3.9	153142	12	US-11-121-086-27		Sequence 27, Appl
c	43	32.2	3.9	201	12	US-11-124-368A-2951		Sequence 2951, Ap
	44	32.2	3.9	425	6	US-09-925-065A-282462		Sequence 282462,
c	45	32.2	3.9	603	6	US-09-925-065A-42254		Sequence 42254, A

ALIGNMENTS

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RESULT 1
US-11-102-978-3/c
; Sequence 3, Application US/11102978
; Publication No. US20050250142A1
; GENERAL INFORMATION:
;  APPLICANT: University of Utah Technology Transfer Office
;  APPLICANT: University of Utah Research Foundation
;  TITLE OF INVENTION: Diagnosis and Treatment of Herpes Simplex Virus Disease
;  FILE REFERENCE: 0274-5537.1US
;  CURRENT APPLICATION NUMBER: US/11/102,978
;  CURRENT FILING DATE:  2005-04-11
;  PRIOR APPLICATION NUMBER: PCT/US2003/033152
;  PRIOR FILING DATE: 2003-10-18
;  PRIOR APPLICATION NUMBER: 60/419,576
;  PRIOR FILING DATE: 2002-10-18
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
;  LENGTH: 340000
;  TYPE: DNA
;  ORGANISM: Homo sapiens
;  FEATURE:
;  NAME/KEY: exon
;  LOCATION: (56948)..(57115)
;  OTHER INFORMATION: C21orf34 exon
;  FEATURE:
;  NAME/KEY: misc_feature
;  LOCATION: (80006)..(81089)
;  OTHER INFORMATION: Gene VDAC2P; voltage-dependent anion channel isoform 2 pseudogene
;  FEATURE:
;  NAME/KEY: exon
;  LOCATION: (167308)..(167438)
;  OTHER INFORMATION: C21orf34 exon
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;  NAME/KEY: exon
;  LOCATION: (216732)..(216833)
;  OTHER INFORMATION: C21orf34 exon
US-11-102-978-3

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Qy    735 CCGAGCTGCA 744
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RESULT 2
US-10-750-185-54718
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; Publication No. US20050260603A1
; GENERAL INFORMATION:
;   APPLICANT: MMI GENOMICS, INC.
;   APPLICANT: DeNISE, Sue K.
;   APPLICANT: KERR, Richard
;   APPLICANT: ROSENFELD, David
;   APPLICANT: HOLM, Tom
;   APPLICANT: BATES, Stephen
;   APPLICANT: FANTIN, Dennis
;   TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
;   FILE REFERENCE: MMI1100-2
;   CURRENT APPLICATION NUMBER: US/10/750,185
;   CURRENT FILING DATE: 2003-12-31
;   PRIOR APPLICATION NUMBER: US 60/437,482
;   PRIOR FILING DATE: 2002-12-31
;   NUMBER OF SEQ ID NOS: 64922
;   SOFTWARE: PatentIn version 3.1
; SEQ ID NO 54718
;   LENGTH: 1285
;   TYPE: DNA
;   ORGANISM: Bovine 1986680902223
US-10-750-185-54718

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Best Local Similarity   53.7%; Pred. No. 7.9;
Matches   72; Conservative   0; Mismatches   62; Indels   0; Gaps   0;

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Qy   47 CTGCTTCCTGTAGGCCCTCTGGGCAGAAGCATGCGCTGGTGTCTCCTCCTGATCTCGGGCC 106
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RESULT 3
US-10-750-623-54718
; Sequence 54718, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
;   APPLICANT: MMI GENOMICS, INC.
;   APPLICANT: DeNISE, Sue K.
;   APPLICANT: KERR, Richard
;   APPLICANT: ROSENFELD, David
;   APPLICANT: HOLM, Tom
;   APPLICANT: BATES, Stephen
;   APPLICANT: FANTIN, Dennis
;   TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
;   FILE REFERENCE: MMI1100-1
;   CURRENT APPLICATION NUMBER: US/10/750,623
;   CURRENT FILING DATE: 2003-12-31
;   PRIOR APPLICATION NUMBER: US 60/437,482

; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 54718
; LENGTH: 1285
; TYPE: DNA
; ORGANISM: Bovine 1986680902223
US-10-750-623-54718

Query Match   4.2%; Score 34.8; DB 8; Length 1285;
Best Local Similarity   53.7%; Pred. No. 7.9;
Matches   72; Conservative   0; Mismatches   62; Indels   0; Gaps   0;

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Db  169 CAGACCAATAAAGC 182
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RESULT 4
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; Sequence 49, Application US/10689742
; Publication No. US20050250180A1
; GENERAL INFORMATION:
;   APPLICANT: Jacobs, Kenneth
;   APPLICANT: McCoy, John M
;   APPLICANT: LaVallie, Edward R
;   APPLICANT: Racie, Lisa A
;   APPLICANT: Evans, Cheryl
;   APPLICANT: Merberg, David
;   APPLICANT: Treacy, Maurice
;   APPLICANT: Spaulding, Vikki
;   TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
;   FILE REFERENCE: 00766.000091.10
;   CURRENT APPLICATION NUMBER: US/10/689,742
;   CURRENT FILING DATE: 2003-10-22
;   PRIOR APPLICATION NUMBER: 09/746,783
;   PRIOR FILING DATE: 2000-12-21
;   NUMBER OF SEQ ID NOS: 231
;   SOFTWARE: PatentIn version 3.2
; SEQ ID NO 49
;   LENGTH: 1694
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-689-742-49

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Best Local Similarity   60.6%; Pred. No. 8.5;
Matches   37; Conservative   0; Mismatches   37; Indels   0; Gaps   0;

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Qy  183 AGAAAGGTGGCTCTATCATCTTACAATGTCACCT 216
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RESULT 5
US-10-947-249-189
; Sequence 189, Application US/10947249
; Publication No. US20050287541A1
; GENERAL INFORMATION:
;   APPLICANT: Akira NAKAGAWARA
;   APPLICANT: Miki OHIRA

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                    GenCore version 5.1.7
        Copyright (c) 1993 - 2006  Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on:    March  4, 2006, 05:57:23 ; Search time 230 Seconds
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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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           2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                         SUMMARIES
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3	756	58.8	150	2	Q6MZS2_HUMAN	Q6mzs2 homo sapien
4	140.5	10.9	510	2	Q96NY8_HUMAN	Q96ny8 homo sapien
5	138	10.7	508	2	Q8CED8_MOUSE	Q8ced8 mus musculu
6	137	10.7	483	2	Q9DBP8_MOUSE	Q9dbp8 mus musculu
7	137	10.7	508	2	Q8R007_MOUSE	Q8r007 mus musculu
8	133.5	10.4	510	2	Q96K15_HUMAN	Q96k15 homo sapien
9	131.5	10.2	510	2	Q5E929_BOVIN	Q5e929 bos taurus
10	126	9.8	563	2	Q5FWR8_XENTR	Q5fwr8 xenopus tro
11	125	9.7	336	2	O46551_9PRIM	O46551 hylobates s
12	123.5	9.6	114	2	Q8HYT0_MOGWO	Q8hyt0 mogera wogu
13	123	9.6	105	2	Q8HYT6_RABIT	Q8hyt6 oryctolagus
14	122.5	9.5	467	2	Q8C6F2_MOUSE	Q8c6f2 mus musculu
15	122.5	9.5	530	1	PVR2_MOUSE	Pvr2 mouse
16	122.5	9.5	530	2	Q80XJ5_MOUSE	Q80xj5 mus musculu
17	122.5	9.5	530	2	Q5FVC5_RAT	Q5fvc5 rattus norv
18	122	9.5	159	2	Q7Z458_HUMAN	Q7z458 homo sapien
19	122	9.5	479	2	Q6IBI6_HUMAN	Q6ibi6 homo sapien
20	122	9.5	538	1	PVR2_HUMAN	Q92692 homo sapien
21	120	9.3	215	2	Q6T3V1_CTEID	Q6t3v1 ctenopharyn
22	118.5	9.2	336	1	CD226_HUMAN	O15762 homo sapien
23	118	9.2	1209	2	Q4SFS8_TETNG	Q48f88 tetraodon n
24	117	9.1	483	2	Q4RRK0_TETNG	Q4rrk0 tetraodon n
25	117	9.1	485	2	Q4RRC2_TETNG	Q4rrc2 tetraodon n
26	116.5	9.1	114	2	Q8HYU0_BOVIN	Q8hyu0 bos taurus
27	116.5	9.1	467	2	Q91VT9_MOUSE	Q91vt9 mus musculu
28	115.5	9.0	114	2	Q8HYT2_TURTR	Q8hyt2 tursiops tr
29	115.5	9.0	463	2	Q66J72_XENLA	Q66j72 xenopus lae
30	114.5	8.9	254	2	Q52ZKJ6_CHICK	Q5zkj6 gallus gall
31	113.5	8.8	1165	2	Q5U5A3_XENLA	Q5u5a3 xenopus lae
32	113	8.8	267	2	Q8NC05_HUMAN	Q8nc05 homo sapien
33	113	8.8	306	2	Q4SMD1_TETNG	Q4smd1 tetraodon n
34	113	8.8	345	2	Q5ZKS7_CHICK	Q5zks7 gallus gall
35	113	8.8	412	2	Q8HY14_RABIT	Q8hy14 oryctolagus
36	113	8.8	515	2	PVR1_MOUSE	Q9jkf6 mus musculu
37	113	8.8	515	2	Q6P9M9_MOUSE	Q6p9m9 mus musculu
38	113	8.8	588	2	Q6IR66_XENLA	Q6ir66 xenopus lae
39	112.5	8.7	114	2	Q8HYT4_CANFA	Q8hyt4 canis faml
40	112.5	8.7	449	2	Q9UEI6_HUMAN	Q9uei6 homo sapien
41	112	8.7	336	1	CD226_MACMU	O18906 macaca mula
42	111.5	8.7	220	2	Q8K4E3_MOUSE	Q8k4e3 mus musculu
43	111.5	8.7	333	1	CD226_MOUSE	Q8k4f0 mus musculu
44	111.5	8.7	333	2	Q5DW69_MOUSE	Q5dw69 mus musculu
45	111	8.6	190	2	Q4S8A2_TETNG	Q4s8a2 tetraodon n

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                           ALIGNMENTS

RESULT 1
Q5JPD8_HUMAN
ID   Q5JPD8_HUMAN PRELIMINARY;       PRT;    311 AA.
AC   Q5JPD8;
DT   10-MAY-2005 (TrEMBLrel. 30, Created)
DT   10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   Hypothetical protein DKFZp667A205.
GN   Name=DKFZp667A205;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Lymph node;
RG   The German cDNA Consortium;
RA   Bloecker H., Boecher M., Brandt P., Mewes H.W., Weil B., Amid C.,
RA   Osanger A., Fobo G., Han M., Wiemann S.;
RL   Submitted (JAN-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AL833175; CAI46183.1; -; mRNA.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   SMART; SM00409; IG; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Hypothetical protein; Immunoglobulin domain.
SQ   SEQUENCE   311 AA;  33926 MW;  AA9E93944DCB3EB CRC64;

Query Match            100.0%;   Score 1286;   DB 2;  Length 311;
Best Local Similarity  100.0%;   Pred. No. 3e-103;
Matches  244;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy     1  MRWCLLIWAQGLRQAPLASGMMTGTIETTGNISAEKGGSIILQCHLSSTTAQVTQVNWE   60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    68  MRWCLLIWAQGLRQAPLASGMMTGTIETTGNISAEKGGSIILQCHLSSTTAQVTQVNWE  127

Qy    61  QQDQLLAICNADLGWHISPSFKDRVAPGPLGLTQSLTVNDTGEYFCIYHTYPDGTYTG  120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   128  QQDQLLAICNADLGWHISPSFKDRVAPGPLGLTQSLTVNDTGEYFCIYHTYPDGTYTG  187

Qy   121  RIFLEVLESSVAEHGARFQIPLLGAMAATLVVICTAVIVVALTRKKKALRIHSVEGDLR  180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   188  RIFLEVLESSVAEHGARFQIPLLGAMAATLVVICTAVIVVALTRKKKALRIHSVEGDLR  247

Qy   181  RKSAGQEEWSPSAPSPPGSCVQAEAAPAGLCGEQRGEDCAELHDYFNVLSYRSLGNCSFF  240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   248  RKSAGQEEWSPSAPSPPGSCVQAEAAPAGLCGEQRGEDCAELHDYFNVLSYRSLGNCSFF  307

Qy   241  TETG  244
          ||||
Db   308  TETG  311
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Qy  181 RKSAGQEEWSPSAPSPPGSCVQAEAAPAGLCGEQRGEDCAELHDYFNVLSYRSLGNCSFF 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 RKSAGQEEWSPSAPSPPGSCVQAEAAPAGLCGEQRGEDCAELHDYFNVLSYRSLGNCSFF 240

Qy  241 TETG 244
        ||||
Db  241 TETG 244
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RESULT 3
Q6MZS2_HUMAN
ID   Q6MZS2_HUMAN PRELIMINARY;   PRT;   150 AA.
AC   Q6MZS2;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein DKFZp667N0215 (Fragment).
GN   Name=DKFZp667N0215;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Lymph node;
RG   The German Human cDNA Consortium;
RA   Ottenwaelder B., Obermaier B., Deutschenbaur S., Mewes H.W., Weil B.,
RA   Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
RL   Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BX640915; CAE45956.1; -; mRNA.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   SMART; SM00409; IG; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Hypothetical protein.
FT   NON_TER   1   1
SQ   SEQUENCE   150 AA; 16123 MW; E4756449EBC92482 CRC64;

Query Match   58.8%; Score 756; DB 2; Length 150;
Best Local Similarity   100.0%; Pred. No. 1.4e-57;
Matches 146; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy   21 GMMTGTIETTGNISAEKGGSIILQCHLSSTTAQVTQVNWEQQDQLLAICNADLGWHISPS 80
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 GMMTGTIETTGNISAEKGGSIILQCHLSSTTAQVTQVNWEQQDQLLAICNADLGWHISPS 60

Qy   81 FKDRVAPGPGLGLTLQSLTVNDTGEYFCIYHTYPDGTYTGRIFLEVLESSVAEHGARFQI 140
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 FKDRVAPGPGLGLTLQSLTVNDTGEYFCIYHTYPDGTYTGRIFLEVLESSVAEHGARFQI 120

Qy  141 PLLGAMAATLVVICTAVIVVVALTRK 166
         |||||||||||||||||||||||||
Db  121 PLLGAMAATLVVICTAVIVVVALTRK 146
```

RESULT 4
Q96NY8_HUMAN
ID   Q96NY8_HUMAN PRELIMINARY;   PRT;   510 AA.
AC   Q96NY8;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Nectin 4 (PVRL4 protein) (Poliovirus receptor-related 4).
GN   Name=PVRL4; ORFNames=RP11-544M22.7-001;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=21560925; PubMed=11544254; DOI=10.1074/jbc.M103810200;

RESULT 2
Q8N877_HUMAN
ID   Q8N877_HUMAN PRELIMINARY;   PRT;   244 AA.
AC   Q8N877;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein FLJ39873.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Spleen;
RX   PubMed=14702039; DOI=10.1038/ng1285;
RA   Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA   Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA   Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA   Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,
RA   Nagahari K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,
RA   Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,
RA   Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,
RA   Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M.,
RA   Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,
RA   Fujimori K., Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y.,
RA   Ishida S., Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T.,
RA   Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,
RA   Nomura N., Togiya S., Komai F., Hara R., Takeuchi K., Arita M.,
RA   Imose N., Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA   Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA   Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA   Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA   Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA   Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA   Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA   Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
RA   Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA   Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA   Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA   Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
RA   Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA   Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA   Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
RT   "Complete sequencing and characterization of 21,243 full-length human
RT   cDNAs.";
RL   Nat. Genet. 36:40-45(2004).
DR   EMBL; AK097192; BAC04973.1; -; mRNA.
DR   Ensembl; ENSG00000181847; Homo sapiens.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   SMART; SM00409; IG; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Immunoglobulin domain.
SQ   SEQUENCE   244 AA; 26289 MW; F98CDF73F604B858 CRC64;

Query Match   99.6%; Score 1281; DB 2; Length 244;
Best Local Similarity   99.6%; Pred. No. 6.1e-103;
Matches 243; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

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Qy    1 MRWCLLLIWAQGLRQAPLASGMMTGTIETTGNISAEKGGSIILQCHLSSTTAQVTQVNWE 60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MRWCLLLIWAQGLRQAPLASGMMTGTIETTGNISAEKGGSIILQCHLSSTTAQVTQVNWE 60

Qy   61 QQDQLLAICNADLGWHISPSFKDRVAPGPGLGLTLQSLTVNDTGEYFCIYHTYPDGTYTG 120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 QQDQLLAICNADLGWHISPSFKDRVAPGPGLGLTLQSLTVNDTGEYFCIYHTYPDGAYTG 120

Qy  121 RIFLEVLESSVAEHGARFQIPLLGAMAATLVVICTAVIVVVALTRKKKALRIHSVEGDLR 180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 RIFLEVLESSVAEHGARFQIPLLGAMAATLVVICTAVIVVVALTRKKKALRIHSVEGDLR 180
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              GenCore version 5.1.7
         Copyright (c) 1993 - 2006  Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on:     March  4, 2006, 05:56:48 ; Search time 188 Seconds
                                        (without alignments)
                                        570.258 Million cell updates/sec

Title:           US-10-658-482-2
Perfect score:   1286
Sequence:        1 MRWCLLLIWAQGLRQAPLAS........YFNVLSYRSLGNCSFFTETG 244

Scoring table:   BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched:        243163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters:      2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       A_Geneseq_21:*
           1: geneseqp19808:*
           2: geneseqp19908:*
           3: geneseqp20008:*
           4: geneseqp20018:*
           5: geneseqp20028:*
           6: geneseqp20038:*
           7: geneseqp2003a8:*
           8: geneseqp2003b8:*
           9: geneseqp20048:*
           9: geneseqp20058:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1286	100.0	1286	8	ADM32156.	Adm32156 PROS2254
2	1286	100.0	244	8	ADL91492	Adl91492 Human imm
3	1286	100.0	257	7	ADF76825	Adf76825 Novel hum
4	1286	100.0	311	6	ADA21139	Ada21139 Human sec
5	1281	99.6	244	7	ADM05498	Adm05498 Human pro
6	1254.5	97.6	249	7	ADE07984	Ade07984 Novel pro
7	1254.5	97.6	249	6	ADU40354	Adu40354 Novel hum
8	1178.5	91.6	240	7	ADE09032	Ade09032 Novel pro
9	707.5	55.0	241	8	ADM32158	Adm32158 Mouse PRO
10	492.5	38.3	98	5	AAG81431	Aag81431 Human AFP
11	256	19.9	50	5	ABP10156	Abp10156 Human ORF
12	146.5	11.4	498	5	AAE23305	Aae23305 Human nec
13	140.5	10.9	485	8	ADK83283	Adk83283 Human 191
14	140.5	10.9	485	8	ADK83298	Adk83298 Human 191
15	140.5	10.9	485	8	ADK83184	Adk83184 Human 191
16	140.5	10.9	485	8	ADK83202	Adk83202 Human 191
17	140.5	10.9	485	8	ADK83285	Adk83285 Human 191
18	140.5	10.9	497	5	AAE23303	Aae23303 Human nec
19	140.5	10.9	510	5	AAU00471	Aau00471 Human TAN
20	140.5	10.9	510	5	ABJ05562	Abj05562 Breast ca
21	140.5	10.9	510	6	ABR48229	Abr48229 Human bla
22	140.5	10.9	510	6	ABU56613	Abu56613 Lung canc
23	140.5	10.9	510	6	ABP97212	Abp97212 Tumour-as
24	140.5	10.9	510	7	ADB80512	Adb80512 Ovarian c
25	140.5	10.9	510	7	ADM42033	Adm42033 Human TAN
26	140.5	10.9	510	7	ADN38748	Adn38748 Cancer/an
27	140.5	10.9	510	8	ADK83210	Adk83210 Human Ig
28	140.5	10.9	510	8	ADK83290	Adk83290 Human 191
29	140.5	10.9	510	8	ADK83209	Adk83209 Human 191
30	140.5	10.9	510	8	ADK83284	Adk83284 Human 191
31	140.5	10.9	510	8	ADK83172	Adk83172 Human 191
32	140.5	10.9	510	8	ADK83174	Adk83174 Human 191
33	140.5	10.9	510	8	ADK83176	Adk83176 Human 191
34	140.5	10.9	510	8	ADK83194	Adk83194 Human 191
35	140.5	10.9	510	8	ADK83180	Adk83180 Human 191
36	140.5	10.9	510	8	ADK83291	Adk83291 Human 191
37	140.5	10.9	510	8	ADK83200	Adk83200 Human 191
38	140.5	10.9	510	8	ADK83199	Adk83199 Human 191
39	140.5	10.9	510	8	ADK83205	Adk83205 Human 191
40	140.5	10.9	510	8	ADK83251	Adk83251 Human 191
41	140.5	10.9	510	8	ADK83289	Adk83289 Human 191
42	140.5	10.9	510	8	ADK83296	Adk83296 Human 191
43	140.5	10.9	510	8	ADK83186	Adk83186 Human 191
44	140.5	10.9	510	8	ADK83178	Adk83178 Human 191
45	140.5	10.9	510	8	ADK83211	Adk83211 Human 191

ALIGNMENTS

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RESULT 1
ADM32156
ID   ADM32156 standard; protein; 244 AA.
XX
AC   ADM32156;
XX
DT   17-JUN-2004  (first entry)
XX
DE   PROS2254 amino acid sequence, seq id 2.
XX
KW   Immunosuppressive; dermatological; hepatotropic; nephrotropic;
KW   antidiabetic; antiasthmatic; antipsoriatic; antiallergic; antianaemic;
KW   antiarteriosclerotic; antiarthritic; neuroprotective; respiratory;
KW   antiinflammatory; gene therapy; rheumatoid arthritis; asthma.
XX
OS   Unidentified.
XX
PN   WO2004024068-A2.
XX
PD   25-MAR-2004.
XX
PF   '09-SEP-2003; 2003WO-US028202.
XX
PR   11-SEP-2002; 2002US-0410062P.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Baldwin DT, Bodary SC, Chan AC, Clark H, Jackman JK, Wood WI;
XX
DR   WPI; 2004-269871/25.
DR   N-PSDB; ADM32155.
XX
PT   New PROS2254 nucleic acid or polypeptide, useful for preparing a
PT   composition for diagnosing or treating in a mammal an immune related
PT   disorder e.g. systemic lupus erythematosus.
XX
PS   Claim 3; SEQ ID NO 2; 100pp; English.
XX
CC   The invention relates to an isolated PROS2254 nucleic acid. Further
CC   disclosed is a vector comprising the nucleic acid. The PROS2254 nucleic
CC   acid or polypeptide is useful for preparing a composition for diagnosing
CC   or treating an immune related disorder, e.g., systemic lupus
CC   erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic
CC   arthritis, spondyloarthropathy, systemic sclerosis, idiopathic
CC   inflammatory myopathy, Sjogren's syndrome, systemic vasculitis,
CC   sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopaenia,
CC   thyroiditis, diabetes mellitus, immune-mediated renal disease, a
```

CC demyelinating disease of the central or peripheral nervous system,
CC idiopathic demyelinating polyneuropathy, Guillain-Barr syndrome, chronic
CC inflammatory demyelinating polyneuropathy, hepatobiliary disease,
CC infectious or autoimmune chronic active hepatitis, sclerosing cholangitis, inflammatory
CC cirrhosis, granulomatous hepatitis, sclerosing cholangitis, inflammatory
CC bowel disease, gluten-sensitive enteropathy, Whipple's disease,
CC autoimmune or immune-mediated skin disease, bullous skin disease,
CC erythema multiforme, contact dermatitis, psoriasis, allergic disease,
CC asthma, allergic rhinitis, atopic dermatitis, food hypersensitivity,
CC urticaria, immunologic disease of the lung, eosinophilic pneumonias,
CC idiopathic pulmonary fibrosis, hypersensitivity pneumonitis,
CC transplantation associated disease, graft rejection or graft-versus-host-
CC disease. The current sequence represents the PRO52245 amino acid
CC sequence.
XX
SQ Sequence 244 AA;

Query Match   100.0%;   Score 1286; DB 8;   Length 244;
Best Local Similarity 100.0%;   Pred. No. 1.2e-112;
Matches 244; Conservative   0; Mismatches   0; Indels   0;   Gaps   0;

Qy   1 MRWCLLLIWAQGLRQAPLASGMMTGTIETTGNISABKGGSIILQCHLSSTTAQVTQVNWE 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MRWCLLLIWAQGLRQAPLASGMMTGTIETTGNISABKGGSIILQCHLSSTTAQVTQVNWE 60

Qy   61 QQDQLLAICNADLGWHISPSFKDRVAPGPGLGLTLQSLTVNDTGEYFCIYHTYPDGTYTG 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 QQDQLLAICNADLGWHISPSFKDRVAPGPGLGLTLQSLTVNDTGEYFCIYHTYPDGTYTG 120

Qy   121 RIFLEVLESSVAEHGARFQIPLLGAMAATLVVICTAVIVVVALTRKKKALRIHSVEGDLR 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 RIFLEVLESSVAEHGARFQIPLLGAMAATLVVICTAVIVVVALTRKKKALRIHSVEGDLR 180

Qy   181 RKSAGQEEWSPSAPSPPGSCVQAEAAPAGLCGEQRGEDCAELHDYFNVLSYRSLGNCSFF 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 RKSAGQEEWSPSAPSPPGSCVQAEAAPAGLCGEQRGEDCAELHDYFNVLSYRSLGNCSFF 240

Qy   241 TETG 244
          ||||
Db   241 TETG 244

RESULT 2
ADL91492
ID ADL91492 standard; protein; 244 AA.
XX
AC ADL91492;
XX
DT 17-JUN-2004 (first entry)
XX
DE Human immune-related polypeptide PRO52254, SEQ ID NO:7.
XX
KW Human; PRO; activated T cell; immune-related; drug screening; detection;
KW stimulation; immune response; stimulation; diagnosis; immune disorder;
KW systemic lupus erythematosus; rheumatoid arthritis; osteoarthritis;
KW juvenile chronic arthritis; spondyloarthropathy; systemic sclerosis;
KW idiopathic inflammatory myopathy; Sjogren's syndrome;
KW systemic vasculitis; sarcoidosis; autoimmune haemolytic anaemia;
KW autoimmune thrombocytopenia; thyroiditis; diabetes mellitus;
KW immune-mediated renal disease; demyelinating disease;
KW idiopathic demyelinating polyneuropathy; Guillain-Barre syndrome;
KW chronic inflammatory demyelinating polyneuropathy; hepatobiliary disease;
KW chronic active hepatitis; primary biliary cirrhosis;
KW granulomatous hepatitis; sclerosing cholangitis;
KW inflammatory bowel disease; gluten-sensitive enteropathy;
KW Whipple's disease; autoimmune skin disease; immune-mediated skin disease;
KW bullous skin disease; erythema multiforme; contact dermatitis; psoriasis;
KW allergic disease; asthma; allergic rhinitis; atopic dermatitis;
KW food hypersensitivity; urticaria; eosinophilic pneumonia;
KW idiopathic pulmonary fibrosis; hypersensitivity pneumonitis;
KW transplantation associated disease; graft rejection;
KW graft-versus-host-disease; immunosuppressive; dermatological;
KW hepatotropic; nephrotropic; antidiabetic; antiasthmatic; antipsoriatic;

KW antiallergic; antianaemic; antiarteriosclerotic; antiarthritic;
KW neuroprotective; respiratory; antiinflammatory; gene therapy.
XX
OS Homo sapiens.
XX
PN WO200404072-A2.
XX
PD 25-MAR-2004.
XX
PF 10-SEP-2003; 2003WO-US028317.
XX
PR 11-SEP-2002; 2002US-0410340P.
XX
PA (GETH) GENENTECH INC.
XX
PI Bodary SC, Clark H, Hunte B,   Jackman JK,   Schoenfeld JR;
PI Williams PM, Wood WI,   Wu TD;
XX
DR WPI; 2004-329384/30.
DR N-PSDB; ADL91491.
XX
PT New PRO nucleic acid, useful for preparing a composition for diagnosing
PT or treating an immune related disorder, e.g., systemic lupus
PT erythematosus in a mammal.
XX
PS Claim 10; SEQ ID NO 7; 199pp; English.
XX
CC The invention relates to isolated human immune-related polypeptides
CC (designated PRO) and nucleic acids (ADL91486-ADL91587). The PRO
CC polypeptides are overexpressed in CD4+ T cells activated by anti-CD3/ICAM
CC -1 or anti-CD3/anti-CD28 antibodies compared with resting T cells and are
CC useful as diagnostic markers and therapeutic targets for immune
CC disorders. The invention also relates to sequences at least 80% identical
CC to the PRO nucleic acid and polypeptide sequences of the invention;
CC recombinant vectors and host cells comprising a PRO nucleic acid; a
CC method for the recombinant production of a PRO polypeptide; antibodies
CC against a PRO polypeptide; fusion proteins comprising a PRO polypeptide;
CC methods of screening for compounds which modulate PRO polypeptide
CC activity or expression; a method for detecting a PRO polypeptide; a
CC method of detecting an immune response in a mammal; a method for
CC stimulating an immune response in a mammal; and methods for diagnosing
CC and treating immune-related disorders. PRO polypeptides and nucleic acids
CC are useful in the diagnosis and treatment of immune-related disorders
CC such as systemic lupus erythematosus, rheumatoid arthritis,
CC osteoarthritis, juvenile chronic arthritis, spondyloarthropathy, systemic
CC sclerosis, idiopathic inflammatory myopathy, Sjogren's syndrome, systemic
CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
CC thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal
CC disease, a demyelinating disease of the central or peripheral nervous
CC system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome,
CC chronic inflammatory demyelinating polyneuropathy, hepatobiliary disease,
CC infectious or autoimmune chronic active hepatitis, primary biliary
CC cirrhosis, granulomatous hepatitis, sclerosing cholangitis, inflammatory
CC bowel disease, gluten-sensitive enteropathy, Whipple's disease,
CC autoimmune or immune-mediated skin disease, bullous skin disease,
CC erythema multiforme, contact dermatitis, psoriasis, allergic disease,
CC asthma, allergic rhinitis, atopic dermatitis, food hypersensitivity,
CC urticaria, immunologic disease of the lung, eosinophilic pneumonias,
CC idiopathic pulmonary fibrosis, hypersensitivity pneumonitis,
CC transplantation associated disease, graft rejection or graft-versus-host-
CC disease. The present sequence represents a human immune-related PRO
CC polypeptide of the invention.
XX
SQ Sequence 244 AA;

Query Match   100.0%;   Score 1286; DB 8;   Length 244;
Best Local Similarity 100.0%;   Pred. No. 1.2e-112;
Matches 244; Conservative   0; Mismatches   0; Indels   0;   Gaps   0;

Qy   1 MRWCLLLIWAQGLRQAPLASGMMTGTIETTGNISABKGGSIILQCHLSSTTAQVTQVNWE 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MRWCLLLIWAQGLRQAPLASGMMTGTIETTGNISABKGGSIILQCHLSSTTAQVTQVNWE 60

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                    GenCore version 5.1.7
            Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on:      March  4, 2006, 06:05:04 ; Search time 166 Seconds
                                        (without alignments)
                                        614.159 Million cell updates/sec

Title:       US-10-658-482-2
Perfect score: 1286
Sequence:    1 MRWCLLLIWAQGLRQAPLAS.........YFNVLSYRSLGNCSFFTETG 244

Scoring table: BLOSUM62
             Gapop 10.0 , Gapext 0.5

Searched:    1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters:      1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published Applications_AA_Main:*
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             2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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             4: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
             5: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
             6: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
             7: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                              SUMMARIES

                  %
Result        Query
No.    Score  Match Length DB ID                        Description
----   -----  ----- ------ -- --                        -----------
  1    1286   100.0  257   5  US-10-370-715B-500         Sequence 500, App
  2    1281    99.6  244   5  US-10-108-260A-4183        Sequence 4183, Ap
  3    1254.5  97.6  249   5  US-10-128-558-139          Sequence 139, App
  4     146.5  11.4  498   3  US-09-972-268-39           Sequence 39, Appl
  5     140.5  10.9  485   4  US-10-422-571-15           Sequence 15, Appl
  6     140.5  10.9  485   4  US-10-422-571-33           Sequence 33, Appl
  7     140.5  10.9  485   4  US-10-422-571-114          Sequence 114, App
  8     140.5  10.9  485   4  US-10-422-571-116          Sequence 116, App
  9     140.5  10.9  485   4  US-10-422-571-129          Sequence 129, App
 10     140.5  10.9  497   3  US-09-972-268-37           Sequence 37, Appl
 11     140.5  10.9  510   4  US-09-766-511B-33          Sequence 33, Appl
 12     140.5  10.9  510   4  US-10-241-220-94           Sequence 94, Appl
 13     140.5  10.9  510   4  US-10-295-027-66           Sequence 66, Appl
 14     140.5  10.9  510   4  US-10-173-999-76           Sequence 76, Appl
 15     140.5  10.9  510   4  US-10-058-270A-54          Sequence 54, Appl
 16     140.5  10.9  510   4  US-10-188-832-179          Sequence 179, App
 17     140.5  10.9  510   4  US-10-422-571-3            Sequence 3, Appli
 18     140.5  10.9  510   4  US-10-422-571-5            Sequence 5, Appli
 19     140.5  10.9  510   4  US-10-422-571-7            Sequence 7, Appli
 20     140.5  10.9  510   4  US-10-422-571-9            Sequence 9, Appli
 21     140.5  10.9  510   4  US-10-422-571-11           Sequence 11, Appl
 22     140.5  10.9  510   4  US-10-422-571-17           Sequence 17, Appl
 23     140.5  10.9  510   4  US-10-422-571-25           Sequence 25, Appl
 24     140.5  10.9  510   4  US-10-422-571-30           Sequence 30, Appl
 25     140.5  10.9  510   4  US-10-422-571-31           Sequence 31, Appl
 26     140.5  10.9  510   4  US-10-422-571-36           Sequence 36, Appl
 27     140.5  10.9  510   4  US-10-422-571-40           Sequence 40, Appl
 28     140.5  10.9  510   4  US-10-422-571-41           Sequence 41, Appl
 29     140.5  10.9  510   4  US-10-422-571-42           Sequence 42, Appl
 30     140.5  10.9  510   4  US-10-422-571-82           Sequence 82, Appl
 31     140.5  10.9  510   4  US-10-422-571-115          Sequence 115, App
 32     140.5  10.9  510   4  US-10-422-571-120          Sequence 120, App
 33     140.5  10.9  510   4  US-10-422-571-121          Sequence 121, App
 34     140.5  10.9  510   4  US-10-422-571-122          Sequence 122, App
 35     140.5  10.9  510   5  US-10-872-972-94           Sequence 94, Appl
 36     140.5  10.9  510   5  US-10-872-972-127          Sequence 127, App
 37     140.5  10.9  511   4  US-10-991-994                Sequence 94, Appl
 38     140.5  10.9  511   4  US-10-422-571-27           Sequence 27, Appl
 39     140.5  10.9  511   4  US-10-422-571-37           Sequence 37, Appl
 40     138.5  10.8  510   3  US-09-97-268-24            Sequence 24, Appl
 41     138.5  10.8  510   3  US-09-829-472A-6           Sequence 6, Appli
 42     138.5  10.8  510   4  US-10-161-572-54           Sequence 54, Appl
 43     138.5  10.8  510   4  US-10-422-571-23           Sequence 23, Appl
 44     138.5  10.8  511   4  US-10-422-571-35           Sequence 35, Appl
 45     137.5  10.7  511   3  US-09-972-268-34           Sequence 34, Appl
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                              ALIGNMENTS

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RESULT 1
US-10-370-715B-500
; Sequence 500, Application US/10370715B
; Publication No. US2004025678A1
; GENERAL INFORMATION:
;   Patin Docket Preview
; APPLICANT: BODARY,SARAH C.
; APPLICANT:   CLARK,HILLARY
; APPLICANT:   BRISDELL,HUNTE
; APPLICANT:   JACKMAN,JANET
; APPLICANT:   SCHOENFELD,JILL R.
; APPLICANT:   WILLIAMS,P. MICKEY
; APPLICANT:   WOOD,WILLIAM I.
; APPLICANT:   WU,THOMAS D.
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Immune
; TITLE OF INVENTION:  Related Diseases
; FILE REFERENCE: P1948R1-US
; CURRENT APPLICATION NUMBER: US/10/370,715B
; CURRENT FILING DATE:  2003-02-21
; NUMBER OF SEQ ID NOS: 742
; SEQ ID NO 500
;  LENGTH: 257
;  TYPE: PRT
;  ORGANISM: Homo sapien
US-10-370-715B-500

Query Match        100.0%;  Score 1286;  DB 5;  Length 257;
Best Local Similarity  100.0%;  Pred. No. 1.7e-107;
Matches  244;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy      1  MRWCLLLIWAQGLRQAPLASGMWTGTIETTGNISAEKGGSIILQCHLSSTTAQVTQVNWE  60
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Db     14  MRWCLLLIWAQGLRQAPLASGMWTGTIETTGNISAEKGGSIILQCHLSSTTAQVTQVNWE  73

Qy     61  QQDQLLAICNADLGWHISPSFKDRVAPGGLGLTLQSLTVNDTGEYFCIYHTYPDGTYTG  120
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Db     74  QQDQLLAICNADLGWHISPSFKDRVAPGGLGLTLQSLTVNDTGEYFCIYHTYPDGTYTG  133

Qy    121  RIFLEVLESSVABHGARFQIPLLGAMAATLVVICTAVIVVALTRKKKALRIHSVEGDLR  180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    134  RIFLEVLESSVABHGARFQIPLLGAMAATLVVICTAVIVVALTRKKKALRIHSVEGDLR  193

Qy    181  RKSAGQEEWSPSAPSPPPGSCVQAEAAPAGLCGEQRGEDCAELHDYFNVLSYRSLGNCSFF  240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    194  RKSAGQEEWSPSAPSPPPGSCVQAEAAPAGLCGEQRGEDCAELHDYFNVLSYRSLGNCSFF  253

Qy    241  TETG  244
           ||||
Db    254  TETG  257
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RESULT 2
US-10-108-260A-4183
; Sequence 4183, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: NO. US2004005560A1e1 full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4183
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Homo sapiens
Us-10-108-260A-4183

Query Match   99.6%; Score 1281; DB 4; Length 244;
Best Local Similarity   99.6%; Pred. No. 4.6e-107;
Matches 243; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

Qy   1 MRWCLLLIWAQGLRQAPLASGMWTGTIETTGNISAEKGGSIILQCHLSSTTAQVTQVNWE 60
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Db   1 MRWCLLLIWAQGLRQAPLASGMWTGTIETTGNISAEKGGSIILQCHLSSTTAQVTQVNWE 60

Qy   61 QQDQLLAICNADLGWHISPSFKDRVAPGPGLGLTIQSLTVNDTGEYFCIYHTYPDGTYTG 120
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Db   61 QQDQLLAICNADLGWHISPSFKDRVAPGPGLGLTIQSLTVNDTGEYFCIYHTYPDGAYTG 120

Qy   121 RIFLEVLESSVAEHGARFQIPLLGAMAATLVVICTAVIVVVALTRKKKALRIHSVEGDLR 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 RIFLEVLESSVAEHGARFQIPLLGAMAATLVVICTAVIVVVALTRKKKALRIHSVEGDLR 180

Qy   181 RKSAGQEEWSPSAPSPPGSCVQAEAAPAGLCGEQRGEDCAELHDYFNVLSYRSLGNCSFF 240
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Db   181 RKSAGQEEWSPSAPSPPGSCVQAEAAPAGLCGEQRGEDCAELHDYFNVLSYRSLGNCSFF 240

Qy   241 TETG 244
              ||||
Db   241 TETG 244

RESULT 3
US-10-128-558-139
; Sequence 139, Application US/10128558
; Publication No. US20040219521A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y., Tom
; APPLICANT: Wang, Zhiwei
; APPLICANT: Weng, Gezhi
; APPLICANT: Boyle, Bryan J
; APPLICANT: Dzmanac, Radoje T
; TITLE OF INVENTION: Novel Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 812A
; CURRENT APPLICATION NUMBER: US/10/128,558
; CURRENT FILING DATE: 2002-04-22
; PRIOR APPLICATION NUMBER: US 60/339,453
; PRIOR FILING DATE: 2001-12-11
; PRIOR: FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: PCT/US00/35017
; PRIOR: FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: US 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: PCT/US01/03800
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: US 09/515,126
; PRIOR FILING DATE: 2000-02-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 412
; SOFTWARE: pt_FL_genes Version 6.0
; SEQ ID NO 139
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-128-558-139

Query Match   97.6%; Score 1254.5; DB 5; Length 249;
Best Local Similarity   96.8%; Pred. No. 1.2e-104;
Matches 242; Conservative   1; Mismatches   1; Indels   0; Gaps   2;

Qy   1 MRWCLLLIWAQGLRQAPLASGMWTGTIETTGNISAEKGGSIILQCHLSSTTAQVTQVNWE 60
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Db   1 MRWCLLLIWAQGLRQAPLASGMWTGTIETTGNISAEKGGSIILQCHLSSTTAQVTQVNWE 60

Qy   61 QQDQLLAICNADLGWHISPSFKDRVAPGPGLGLTIQSLTVNDTGEYFCIYHTYPDGTYTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 QQDQLLAICNADLGWHISPSFKDRVAPGPGLGLTIQSLTVNDTGEYFCIYHTYPDGTYTG 120

Qy   121 RIFLEVLESS------VAEHGARFQIPLLGAMAATLVVICTAVIVVVALTRKKKALRIHS 174
              |||||||||| :|||||||||||||||||||||||||||||||||| ||||||||
Db   121 RIFLEVLESSGIPAGAMAEHGARFQIPLLGAMAATLVVICTAVIVVVALTR-KKALRIHS 179

Qy   175 VEGDLRRKSAGQEEWSPSAPSPPGSCVQAEAAPAGLCGEQRGEDCAELHDYFNVLSYRSL 234
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   235 GNCSFFTETG 244
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Db   240 GNCSFFTETG 249

RESULT 4
US-09-972-268-39
; Sequence 39, Application US/09972268
; Publication No. US2003004893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE TH
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 39
; LENGTH: 498
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-972-268-39

Query Match   11.4%; Score 146.5; DB 3; Length 498;
Best Local Similarity   29.0%; Pred. No. 0.0002;
Matches   51; Conservative   23; Mismatches   63; Indels   39; Gaps   7;

Qy   3 WCLLLIWAQGLRQAPLASGMWTGTIETTGNISAEKGGSIILQC-HLSSTTAQVTQVNWEQ 61
              | ||| : :| . :|| :   : :   .   :   : ::
Db   27 WLLLL-----LLLASFAGRCPAGELETSDVVTVVLGQDAKLPCFYRGDSGEQVGQVAWAR 81

Qy   62 QD-----QLLAICNADLGWHISPSFKDRV-APGPGLGL----TLQSLTVNDTGEYFCIY 110

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OM protein - protein search, using sw model

Run on: March 4, 2006, 06:00:28 ; Search time 40 Seconds
(without alignments)
586.922 Million cell updates/sec

Title: US-10-658-482-2
Perfect score: 1286
Sequence: 1 MRWCLLLIWAQGLRQAPLAS.........YFNVLSYRSLGNCSFFTETG 244

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	122.5	9.5	467	1	HLMSP3	poliovirus recepto
2	122.5	9.5	530	2	A53437	poliovirus recepto
3	122	9.5	478	2	I53960	PRR2 alpha - human
4	122	9.5	538	2	I68093	PRR2 delta - human
5	111.5	8.7	518	2	JC4024	poliovirus recepto
6	106.5	8.3	416	2	A54017	colon carcinoma-as
7	104.5	8.1	392	1	RWHUPD	poliovirus recepto
8	104.5	8.1	417	1	RWHUPA	poliovirus recepto
9	104	8.1	186	2	I61783	sodium channel bet
10	104	8.1	215	2	A57843	sodium channel bet
11	101.5	7.9	304	1	RWCHH7	cell surface glyco
12	100	7.8	108	1	KVMS82	Ig kappa chain V r
13	100	7.8	114	2	S22559	Ig heavy chain V r
14	100	7.8	229	2	A20969	Ig kappa chain pre
15	99	7.7	93	2	I47624	Ig heavy chain V-V
16	99	7.7	108	1	KVMS61	Ig kappa chain V r
17	97	7.5	108	1	KVMS06	Ig Y heavy chain (
18	96.5	7.5	572	2	B46529	Ig Y heavy chain (
19	96	7.5	130	2	S08079	immunoglobulin-lik
20	96	7.5	1327	2	T09402	Ig V-region-like B
21	94.5	7.3	398	2	A39371	Ig kappa chain V r
22	94	7.3	108	1	KVMS09	Ig kappa chain V r
23	94	7.3	128	2	S31488	Ig kappa chain pre
24	94	7.3	129	2	A30554	Ig lambda chain pr
25	94	7.3	381	2	I51174	Ig heavy chain - R
26	93.5	7.3	392	2	B44194	poliovirus recepto
27	93.5	7.3	417	2	A44194	poliovirus recepto
28	93	7.2	125	2	S40315	Ig kappa chain - h
29	93	7.2	468	1	B46114	glycoprotein gp13
30	93	7.2	468	1	VGBEEH	glycoprotein gp13
31	92	7.2	103	2	S18731	Ig kappa chain V-J
32	92	7.2	244	2	A40428	nonspecific cross-
33	91.5	7.1	129	1	K1HUWK	Ig kappa chain pre
34	91.5	7.1	569	2	A46462	T cell activation
35	90.5	7.0	129	2	S52792	Ig kappa chain V r
36	89.5	7.0	105	2	S38488	Ig heavy chain - h
37	89.5	7.0	125	2	S40350	Ig kappa chain - h
38	89.5	7.0	345	2	JC1239	opioid-binding pro
39	89	6.9	210	2	S36297	T-cell receptor ga
40	89	6.9	1512	2	T14883	hypothetical prote
41	88.5	6.9	119	2	PH1503	Ig heavy chain V r
42	88.5	6.9	126	2	S40335	Ig kappa chain V-J
43	88.5	6.9	128	2	A26406	Ig kappa chain V r
44	88.5	6.9	268	2	A56446	Ig heavy chain V r
45	88.5	6.9	430	2	I48142	B-lymphocyte antig

ALIGNMENTS

RESULT 1
HLMSP3
poliovirus receptor homolog precursor - mouse
C;Species: Mus musculus domesticus (western European house mouse)
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
C;Accession: A38211
R;Morrison, M.E.; Racaniello, V.R.
J. Virol. 66, 2807-2813, 1992
A;Title: Molecular cloning and expression of a murine homolog of the human poliovirus rec
A;Reference number: A38211; MUID:9219365; PMID:1560525
A;Accession: A38211
A;Molecule type: DNA
A;Residues: 1-467 <MOR>
A;Cross-references: UNIPROT:P32507; UNIPARC:UPI000002B1F6; GB:M80206; NID:g199785; PIDN:A
C;Superfamily: poliovirus receptor; immunoglobulin homology
C;Keywords: duplication; glycoprotein; transmembrane protein
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-467/Product: poliovirus receptor homolog #status predicted <MAT>
F;26-354/Domain: extracellular #status predicted <EXT>
F;47-133/Domain: immunoglobulin homology <IMM1>
F;167-231/Domain: immunoglobulin homology <IMM2>
F;267-322/Domain: immunoglobulin homology <IMM3>
F;355-374/Domain: transmembrane #status predicted <TMN>
F;375-467/Domain: intracellular #status predicted <INT>
F;54-131,174-229,274-320/Disulfide bonds: #status predicted
F;128,138,315/Binding site: carbohydrate (Asn) (covalent) #status predicted

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Query Match      9.5%;  Score 122.5;  DB 1;  Length 467;
Best Local Similarity   26.7%;   Pred. No. 0.014;
Matches  46;  Conservative  21;  Mismatches  56;  Indels  49;  Gaps   7;

Qy     5 LLLIWAQG------LRQAPLASGMWTGTIETTGNISAEKGGSIILQCH-LSSTTAQVTQVN 58
           |||:  |||:|||  :    |:||
Db    23 LLLLQETGAQDVRVRVLPEVRGRLGGTVE----------------LPCHLLPPTERVSQVT 68

Qy    59 WEQQDQLLAICNADLGWHISPSF------------KDRV----------APGPGLGTLQSL 98
          |: :  |||  : |:|
Db    69 WQRLDGTVVAA------FHPSFGVDFPNSQFSKDRLSFVRARPETNADLRDATLAFRGL 121

Qy    99 TVNDTGEYFCIYHTYPDGTYTGRIFLEVLESSVAEHGARPQIPLLGAMAATL 150
          |: |: |||:|  :  :|  :  :  |:|
Db   122 RVEDEGNYTCBFATFPNGTRRGVTWLRVI--AQPENHAEAQEVTIGPQSVAV 171
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RESULT 2
A53437
poliovirus receptor mPVR - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A53437
R;Aoki, J.; Koike, S.; Ise, I.; Sato-Yoshida, Y.; Nomoto, A.
J. Biol. Chem. 269, 8431-8438, 1994

A;Title: Amino acid residues on human poliovirus receptor involved in interaction with p
A;Reference number: A53437; MUID:94179228; PMID:8132559
A;Accession: A53437
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-530 <AOK>
A;Cross-references: UNIPROT:P32507; UNIPARC:UPI000000271FD; GB:D26107; NID:g475017; PIDN:
A;Experimental source: C57/BL6, brain
A;Note: sequence extracted from NCBI backbone (NCBIN:146664, NCBIP:146667)
C;Genetics:
A;Gene: PRR2alpha
C;Superfamily: immunoglobulin homology
F;276-331/Domain: immunoglobulin homology <IMM>

Query Match   9.5%;   Score 122.5; DB 2; Length 530;
Best Local Similarity 26.7%; Pred. No. 0.016;
Matches 46; Conservative 21; Mismatches 56; Indels 49; Gaps 7;

Qy   5 LLLIWAQG-----LRQAPLASGMWTGTIETTGNISAEKGGSIILQCH-LSSTTAQVTQVN 58
           |||:   :|:||:||:| :.|:||:
Db 23 LLLLQETGAQDVRVRVLPEVRGRLGGTVE----------------LPCHLLPPTTERVSQVT 68

Qy 59 WEQQDQLLAICNADLGWHISPSF---------KDRV----APGPGLGLTLQSL 98
           ||| |||
Db 69 WQRLDGTVVAA-------FHPSFGVDFPNSQFSKDRLSFVRARPETNADLRDATLAFRGL 121

Qy 99 TVNDTGEYFCIYHTYPDGTYTGRIFLEVLESSVAEHGARFQIPLLGAMAATL 150
          |:|||:|||:|:||| :.| :|:|
Db 122 RVEDEGNYTCEFATFPNGTRRGVTWLRVI--AQPENHAERAQEVTIGPQSVAV 171

RESULT 3
I53960
PRR2 alpha - human
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 31-Dec-2004
C;Accession: I53960
R;Eberle, F.; Dubreuil, P.; Mattei, M.G.; Devilard, E.; Lopez, M.
Gene 159, 267-272, 1995
A;Title: The human PRR2 gene, related to the human poliovirus receptor gene (PVR), is th
A;Reference number: I53960; MUID:95347610; PMID:7622062
A;Accession: I53960
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-478 <RES>
A;Cross-references: UNIPROT:Q9UEI6; UNIPARC:UPI00001770B1; GB:S79171; NID:g1042202; PID:
C;Genetics:
A;Gene: PRR2alpha
C;Superfamily: immunoglobulin homology
F;276-331/Domain: immunoglobulin homology <IMM>

Query Match   9.5%;   Score 122;   DB 2; Length 478;
Best Local Similarity 25.2%; Pred. No. 0.016;
Matches 39; Conservative 21; Mismatches 51; Indels 44; Gaps 6;

Qy   3 WCLLLIWAQGLRQAPLASGMWTGTIETTGNISAEKGGSIILQCHLSSTT--AQVTQVNWE 60
           ||||:   :|:||:
Db 19 WPLLLLLL-------LETGAQDVRVQVLPEVRGQLGGTVELPCHLLPPVPGLYISLVTWQ 71

Qy 61 QQD-----QLLAICNADLGWHISPSFKDRVAPGPG-----------------LG 92
           ||| |||:
Db 72 RPDAPANHQNVAAFHPKMG----PSPP---SPKPGSERLSFVSAKQSTGQDTEAELQDAT 124

Qy 93 LTLQSLTVNDTGEYFCIYHTYPDGTYTGRIFLEVL 127
          |||||:|||:|||:|:||| | :|
Db 125 LALHGLTVEDEGNYTCEFATFPKGSVRGMTWLRVI 159

RESULT 4
I68093
PRR2 delta - human
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C;Accession: I68093
R;Eberle, F.; Dubreuil, P.; Mattei, M.G.; Devilard, E.; Lopez, M.

Gene 159, 267-272, 1995
A;Title: The human PRR2 gene, related to the human poliovirus receptor gene (PVR), is the
A;Reference number: I53960; MUID:95347610; PMID:7622062
A;Accession: I68093
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-538 <RES>
A;Cross-references: UNIPROT:Q92692; UNIPARC:UPI000004A2BF; GB:S79172; NID:g1042204; PID:S
C;Genetics:
A;Gene: PRR2delta
C;Superfamily: poliovirus receptor; immunoglobulin homology
F;276-331/Domain: immunoglobulin homology <IMM>

Query Match   9.5%;   Score 122;   DB 2; Length 538;
Best Local Similarity 25.2%; Pred. No. 0.018;
Matches 39; Conservative 21; Mismatches 51; Indels 44; Gaps 6;

Qy   3 WCLLLIWAQGLRQAPLASGMWTGTIETTGNISAEKGGSIILQCHLSSTT--AQVTQVNWE 60
           ||||:   :|:||:
Db 19 WPLLLLLL-------LETGAQDVRVQVLPEVRGQLGGTVELPCHLLPPVPGLYISLVTWQ 71

Qy 61 QQD-----QLLAICNADLGWHISPSFKDRVAPGPG-----------------LG 92
           ||| |||:
Db 72 RPDAPANHQNVAAFHPKMG----PSPP---SPKPGSERLSFVSAKQSTGQDTEAELQDAT 124

Qy 93 LTLQSLTVNDTGEYFCIYHTYPDGTYTGRIFLEVL 127
          |||||:|||:|||:|:||| | :|
Db 125 LALHGLTVEDEGNYTCEFATFPKGSVRGMTWLRVI 159

RESULT 5
JC4024
poliovirus receptor-related protein precursor - human
C;Species: Homo sapiens (man)
C;Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 05-Nov-1999
C;Accession: JC4024
R;Lopez, M.; Eberle, F.; Mattei, M.G.; Gabert, J.; Birg, F.; Bardin, F.; Maroc, C.; Dubre
Gene 155, 261-265, 1995
A;Title: Complementary DNA characterization and chromosomal localization of a human gene
A;Reference number: JC4024; MUID:95237621; PMID:7721102
A;Accession: JC4024
A;Molecule type: mRNA
A;Residues: 1-518 <LOP>
A;Cross-references: UNIPARC:UPI00001770B2; EMBL:X76400; NID:g732795; PIDN:CAA53980.1; PII
C;Genetics:
A;Gene: GDB:PVRR1
A;Cross-references: GDB:583951
A;Map position: 11q23-11q24
C;Superfamily: poliovirus receptor; immunoglobulin homology
C;Keywords: glycoprotein; transmembrane protein
F;1-30/Domain: signal sequence #status predicted <SIG>
F;31-518/Product: poliovirus receptor-related protein #status predicted <MAT>
F;356-379/Domain: transmembrane #status predicted <TMM>
F;36,72,82,139,287,308,333/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match   8.7%;   Score 111.5; DB 2; Length 518;
Best Local Similarity 24.4%; Pred. No. 0.13;
Matches 53; Conservative 33; Mismatches 84; Indels 47; Gaps 11;

Qy   2 RWCLLLIW--AQGLRQAPLASGMWTGTIETTGNISAEKGGSIILQCHLSS--TTAQVTQV 57
            || :|:|
Db 12 RW------WGLALGL-TAFFLPGVHSQVVQVNDSMYGFIGTDVVLHCSFANPLPSVKITQV 65

Qy 58 NWEQ----QDQLLAICNADLGWHISPSFKDRV---APGPGLG-LTLQSLTVNDTGEYFCI 109
           :|:   :::| |:|::
Db 66 TWQKSTNGSKQNVAIYNPSMGVSVLAPYRERVEFLRPSFTDGTIRLSRLELEDEGVVICE 125

Qy 110 YHTYPDGTYTGRIFLEV-------LESSVAEHGARFQIPLLGAMAATLVVICTAV----- 157
           |||:|||:|||:| ||:|:| | :|:
Db 126 FATFPTGNRESQLNLTVMAKPTNWIEGTQAVLRAK-----KGQDDKVLVATCTSANGKPP 180

Qy 158 IVVVALTRKKKALRIHSVEGDLRRKSAGQEEWSPSAP 194
           | || || |: ||

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 4, 2006, 06:05:59 ; Search time 20 Seconds
                                        (without alignments)
                                        244.005 Million cell updates/sec

Title: US-10-658-482-2
Perfect score: 1286
Sequence: 1 MRWCLLLIWAQGLRQAPLAS.........YFNVLSYRSLGNCSFFTETG 244

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 135346 seqs, 20000420 residues

Total number of hits satisfying chosen parameters: 135346

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published Applications_AA_New:*
                1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
                2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
                3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
                4: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
                5: /cgn2_6/ptodata/1/pubpaa/US05_NEW_PUB.pep:*
                6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
                7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
                8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	DB	Length	ID	Description
1	140.5	10.9	6	555	US-10-821-234-1015	Sequence 1015, Ap
2	106	8.2	7	7968	US-11-186-731-5	Sequence 5, Appli
3	101	7.9	7	277	US-11-126-817-54	Sequence 54, Appl
4	99	7.7	7	406	US-11-000-463-377	Sequence 377, App
5	99	7.7	7	406	US-11-000-463-849	Sequence 849, App
6	95.5	7.4	6	215	US-10-131-826A-488	Sequence 488, App
7	95.5	7.4	6	215	US-10-973-115B-488	Sequence 488, App
8	95.5	7.4	7	215	US-11-080-991-112	Sequence 112, App
9	94.5	7.3	6	463	US-10-063-703-86	Sequence 86, Appl
10	94.5	7.3	7	463	US-11-102-240-86	Sequence 86, Appl
11	93.5	7.3	7	463	US-11-000-463-872	Sequence 872, App
12	93.5	7.3	7	567	US-11-000-463-400	Sequence 400, App
13	93	7.2	6	269	US-10-131-826A-530	Sequence 530, App
14	93	7.2	6	269	US-10-973-115B-530	Sequence 530, App
15	93	7.2	7	269	US-11-219-146-2	Sequence 2, Appli
16	93	7.2	7	686	US-11-072-175-225	Sequence 225, App
17	92.5	7.2	7	551	US-11-000-463-346	Sequence 346, App
18	91	7.1	7	247	US-11-084-717-23	Sequence 23, Appl
19	91	7.1	7	247	US-11-179-244-23	Sequence 23, Appl
20	91	7.1	7	247	US-11-084-055B-23	Sequence 23, Appl
21	91	7.1	7	269	US-11-219-146-4	Sequence 4, Appli
22	91	7.1	7	269	US-11-219-146-6	Sequence 6, Appli
23	91	7.1	7	269	US-11-219-146-8	Sequence 8, Appli
24	90.5	7.0	7	199	US-11-219-146-42	Sequence 42, Appl
25	90.5	7.0	7	199	US-11-219-146-44	Sequence 44, Appl
26	90.5	7.0	7	209	US-11-219-146-18	Sequence 18, Appl
27	90	7.0	6	107	US-10-946-836A-16	Sequence 16, Appl
28	89.5	7.0	6	107	US-10-988-207-16	Sequence 16, Appl
29	89.5	7.0	6	508	US-10-514-534-7	Sequence 7, Appli
30	89	6.9	7	247	US-11-084-717-25	Sequence 25, Appl
31	89	6.9	7	247	US-11-179-244-25	Sequence 25, Appl
32	89	6.9	6	247	US-11-084-055B-25	Sequence 24, Appl
33	88.5	6.9	7	139	US-11-125-837-24	Sequence 24, Appl
34	88.5	6.9	7	199	US-11-219-146-46	Sequence 46, Appl
35	88.5	6.9	7	199	US-11-219-146-48	Sequence 48, Appl
36	88.5	6.9	7	209	US-11-219-146-20	Sequence 20, Appl
37	88.5	6.9	7	209	US-11-219-146-22	Sequence 22, Appl
38	88.5	6.9	7	236	US-11-086-289-8	Sequence 8, Appli
39	88	6.8	6	135	US-10-993-543-120	Sequence 120, App
40	88	6.8	7	215	US-10-374-954-7	Sequence 7, Appli
41	87.5	6.8	6	288	US-10-821-234-1062	Sequence 1062, Ap
42	87.5	6.8	6	359	US-10-055-877-265	Sequence 265, App
43	87.5	6.8	6	359	US-11-080-091-1	Sequence 1, Appli
44	87.5	6.8	7	359	US-11-116-939-15	Sequence 15, Appl
45	87.5	6.8	7	359	US-11-087-177-23	Sequence 23, Appl

ALIGNMENTS

RESULT 1
US-10-821-234-1015
; Sequence 1015, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_SEQ_genes Version 1.0
; SEQ ID NO 1015
; LENGTH: 555
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1015

Query Match   10.9%; Score 140.5; DB 6; Length 555;
Best Local Similarity   27.3%; Pred. No. 1.3e-05;
Matches   48; Conservative   24; Mismatches   65; Indels   39; Gaps   6;

Qy   3 WCLLLIWAQGLRQAPLASGMMTGTETTGNISAEKGGSIILQC-HLSSTTAQVTQVNWEQ 61
              ||||| | |: |||:|| |||:|
Db   60 WLLLL-----LLLASFTGRCPAGRLETSDVVTTVLGQDAKLPCFYRGDSGEQVGQVAWAR 114

Qy   62 QD-----QLIAICNADLGWHISPSFKDRVAPGP-----GLGLTQSLTVNDTGEYFCIY 110
            || |||: : :|||:|:|||:| ||: |:
Db   115 VDAGEGAQELALLHSKYGLHVSPAYEGRVEQPPPRNPLDGSVLLRNAVQADEGEYECRV 174

Qy   111 HTYPDGTYTGRIFLEVLESSVAEHGARFQIPLLGAM--------AATLVVICTA 156
            :|| |:: |: :| || ||: :|
Db   175 STFPAGSFQARLRLRVL------------------VPPLPSLNPGPALEEGGGLTLAASCTA 218

RESULT 2
US-11-186-731-5
; Sequence 5, Application US/11186731
; Publication No. US20050255521A1
; GENERAL INFORMATION:
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Acton, Susan L.
; TITLE OF INVENTION: 59079 and 12599, Protein Kinase Family

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; TITLE OF INVENTION: Members and Uses Therefor
; FILE REFERENCE: MPI2001-047P1RCP1(M)
; CURRENT APPLICATION NUMBER: US/11/186,731
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/077,130
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: 60/269201
; PRIOR FILING DATE: 2001-02-15
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 7968
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-186-731-5

Query Match      8.2%;   Score 106;  DB 7;  Length 7968;
Best Local Similarity   25.3%;   Pred. No. 0.63;
Matches  55;  Conservative  30;  Mismatches  92;  Indels  40;  Gaps  9;

Qy    27 IETTGNISAEKGGSIILQCHLSSTTAQVTQVNWEQQDQLLAICNADLGWHISPSFKDRVA 86
Db  3805 IEDVRNQEAREGATAVLQCELS----KAAPVEWRKGSETL----------RGGDRYS 3847
Qy    87 ---PGPGLGLTLQSLTVNDTGEYFCIY-HTYPDGTYTGR----IFLEVLESSVAEHGARF 138
Db  3848 LRQDGTRCELQIHGLSVADTGEYSCVCGQERTSATLTVRAPQPVFREPLQSLQREGSTA 3907
Qy   139 QIPLLGAMAATLVVICTAVIVVVALTRKKKALRIHSVE---GDLRRKSAGQEEWSPSAPS 195
Db  3908 TLQCELSEPTATVVWSKGGLQLQANGRREPRLQGCTAELVLQDLQREDTG--EYTCTCGS 3965
Qy   196 PPGSC-VQAEAAPAGLCGEQRGED---------CAEL 222
Db  3966 QATSATLTVTAAPVRFLRELQHQEVDEGGTAHLCCEL 4002

RESULT 3
US-11-126-817-54
; Sequence 54, Application US/11126817
; Publication No. US2006003834A1
; GENERAL INFORMATION:
; APPLICANT: DANA-FARBER CANCER INSTITUTE, INC.
; APPLICANT: MARASCO, Wayne
; APPLICANT: MHASHILKAR, Abner
; TITLE OF INVENTION: INTRABODY-MEDIATED CONTROL OF IMMUNE REACTIONS
; FILE REFERENCE: 47577 C
; CURRENT APPLICATION NUMBER: US/11/126,817
; CURRENT FILING DATE: 2005-05-11
; PRIOR APPLICATION NUMBER: US/09/522,727
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: PCT/US98/19563
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/059,339
; PRIOR FILING DATE: 1997-09-19
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 54
; LENGTH: 277
; TYPE: PRT
; ORGANISM: human
US-11-126-817-54

Query Match      7.9%;   Score 101;  DB 7;  Length 277;
Best Local Similarity   26.8%;   Pred. No. 0.029;
Matches  38;  Conservative  19;  Mismatches  63;  Indels  22;  Gaps  6;

Qy     9 WAQGLRQAPLASGMWTG-----------TIETTGNISAEKGGSIILQCHLSSTTAQVTQ 56
Db   131 WGQGTLVTVSSGGGGSGGGGSGGGGSELVLTQSPSSLSASLGDTITITCHASQNIN--VW 188
Qy    57 VNWEQQ-----DQLLAICNADLGWHISPSFKDRVAPGPGLGLTLQSLTVNDTGEYFCIY- 110
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Db   189 LSWYQQKPGNIPQLLIYKASNLHTGVPSRFSGR-GSGTGFLTITISSLQPEDIGTYYCQQG 247
Qy   111 HTYPDGTYTGRIFLEVLESSVA 132
Db   248 QSYP-LTFGGGTKLEIKRADAA 268

RESULT 4
US-11-000-463-377
; Sequence 377, Application US/11000463
; Publication No. US2005026423A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Chen, Rui-hong
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Zhou, Ping
; APPLICANT: Cao, Yi-Cheng
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 785CIP4CN
; CURRENT APPLICATION NUMBER: US/11/000,463
; CURRENT FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: 10/291,265
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/922,279
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 377
; LENGTH: 406
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-000-463-377

Query Match      7.7%;   Score 99;  DB 7;  Length 406;
Best Local Similarity   24.0%;   Pred. No. 0.072;
Matches  62;  Conservative  33;  Mismatches  87;  Indels  76;  Gaps  15;

Qy     3 WCLLIIWAQGLRQAPLASGMWTGTIETTGNISAEKGGSIILQCHLSSTTAQVTQVNWEQQ 62
Db   155 WNLTMTVFQGDATASTALG-------NGSSLSVLEQSLRLVCAVNSNPP--ARLSWTRG 205
Qy    63 DQLLAICNADLGWHISPSFKDRVAPGPGLGLTLQSLTVNDTGEYFC----------I 109
Db   206 S--LTLC-------PS---RSSNPGL-LELPRVHVRDEGEFTCRAQNAQGSQHISLS 249
Qy   110 YHTYPDGTYTGRIFLEVLESSVAEHGARFQIPLLGAMAATLVVICTAVIVVVALTRKKA 169
Db   250 LSLQNEGTGTSRPVSQVTLAAVG----------GAGATALAFLSPCIFIIVRSCRKKS 298
Qy   170 LRIHSVEGDLR---------RKSAGQ---EEWSPSAP--SPPGSCVQAEAAPAGLCGEORG 216
Db   299 ARPAAGVGDTGMEDAKAIRGSASQGPLTESWKDGNPLKKPPPA-----VAPSS------G 347
Qy   217 EDCAELHDYFNVLSYRSL 234
Db   348 EB-GELH--YATLSFHKV 362
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                GenCore version 5.1.7
        Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on:     March  4, 2006, 06:04:18 ; Search time 47 Seconds
                                       (without alignments)
                                       429.210 Million cell updates/sec

Title:             US-10-658-482-2
Perfect score:     1286
Sequence:          1 MRWCLLLIWAQGLRQAPLAS........YPNVLSYRSLGNCSFFTETG 244

Scoring table:     BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched:          572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters:     572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued Patents AA:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	122	9.5	479	2	US-09-723-368-2	Sequence 2, Appli
2	122	9.5	479	2	US-09-949-016-6278	Sequence 6278, Ap
3	122	9.5	522	2	US-09-949-016-7563	Sequence 7563, Ap
4	111.5	8.7	518	2	US-09-919-172-20	Sequence 20, Appl
5	107	8.3	514	2	US-09-949-016-11380	Sequence 11380, A
6	107	8.3	517	2	US-09-723-368-4	Sequence 4, Appli
7	106	8.2	458	2	US-09-435-956A-1	Sequence 1, Appli
8	105	8.2	408	2	US-09-724-864-62	Sequence 62, Appl
9	104.5	8.1	417	2	US-09-949-016-6729	Sequence 6729, Ap
10	104.5	8.1	456	2	US-09-949-016-7564	Sequence 7564, Ap
11	99.5	7.7	127	1	US-08-137-117D-37	Sequence 37, Appl
12	99.5	7.7	127	1	US-08-436-717-37	Sequence 37, Appl
13	98	7.6	128	1	US-08-379-057-12	Sequence 12, Appl
14	98	7.6	234	2	US-09-740-002-26	Sequence 26, Appl
15	98	7.6	240	2	US-09-049-672A-11	Sequence 11, Appl
16	97	7.5	126	1	US-07-634-278-21	Sequence 21, Appl
17	97	7.5	126	1	US-08-487-728-21	Sequence 21, Appl
18	97	7.5	126	1	US-08-474-040-21	Sequence 21, Appl
19	97	7.5	126	2	US-08-487-200-21	Sequence 21, Appl
20	97	7.5	126	2	US-08-484-537-21	Sequence 21, Appl
21	97	7.5	129	4	PCT-US95-07372-12	Sequence 12, Appl
22	96.5	7.5	551	2	US-08-896-537A-2	Sequence 2, Appli
23	95.5	7.4	215	2	US-09-949-016-6658	Sequence 6658, Ap
24	95.5	7.4	215	2	US-09-991-181-389	Sequence 389, App
25	95.5	7.4	215	2	US-09-990-444-389	Sequence 389, App
26	95.5	7.4	215	2	US-09-997-333-389	Sequence 389, App
27	95.5	7.4	215	2	US-09-992-598-389	Sequence 389, App
28	95.5	7.4	263	2	US-09-949-016-10819	Sequence 10819, A
29	95.5	7.4	354	2	US-09-393-627B-28	Sequence 28, Appl
30	95	7.4	544	2	US-09-999-833A-259	Sequence 259, App
31	95	7.4	544	2	US-10-020-445A-259	Sequence 259, App
32	95	7.4	1011	1	US-08-162-809-12	Sequence 12, Appl
33	94.5	7.3	463	2	US-10-012-231A-160	Sequence 160, App
34	94.5	7.3	463	2	US-10-015-389A-160	Sequence 160, App
35	94.5	7.3	463	2	US-10-006-768A-160	Sequence 160, App
36	94.5	7.3	463	2	US-10-015-671A-160	Sequence 160, App
37	94.5	7.3	463	2	US-10-015-393A-160	Sequence 160, App
38	94.5	7.3	463	2	US-10-011-833A-160	Sequence 160, App
39	94.5	7.3	463	2	US-10-006-041A-160	Sequence 160, App
40	94.5	7.3	463	2	US-10-012-064A-160	Sequence 160, App
41	94.5	7.3	1138	2	US-09-252-991A-20291	Sequence 20291, A
42	93.5	7.3	1248	2	US-09-949-016-10595	Sequence 10595, A
43	93.5	7.3	1248	2	US-09-949-016-10596	Sequence 10596, A
44	93	7.2	269	2	US-09-430-503-2	Sequence 2, Appli
45	93	7.2	269	2	US-10-012-231A-364	Sequence 364, App

ALIGNMENTS

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RESULT 1
US-09-723-368-2
; Sequence 2, Application US/09723368
; Patent No. 6641818
; GENERAL INFORMATION:
;   APPLICANT: NORTHWESTERN UNIVERSITY
;   APPLICANT: SPEAR, Patricia G.
;   APPLICANT: WARNER, Morgyn S.
;   APPLICANT: GERAGHTY, Robert G.
;   APPLICANT: MARTINEZ, Wanda M.
;   APPLICANT: MONTGOMERY, Rebecca I.
;   APPLICANT: COHEN, Gary H.
;   APPLICANT: EISENBERG, Roselyn J.
;   APPLICANT: WHITBECK, Charles J.
;   APPLICANT: KRUMMENACHER, Claude
;   APPLICANT: UNIVERSITY OF PENNSYLVANIA
;   TITLE OF INVENTION: CELLULAR PROTEINS WHICH MEDIATE HERPESVIRUS ENTRY
;   FILE REFERENCE: 200290.0050/2U1
;   CURRENT APPLICATION NUMBER: US/09/723,368
;   CURRENT FILING DATE: 2000-11-28
;   PRIOR APPLICATION NUMBER: U.S. 60/087,862
;   PRIOR FILING DATE: 1998-06-03
;   PRIOR APPLICATION NUMBER: PCT/US99/12235
;   PRIOR FILING DATE: 1999-06-02
;   NUMBER OF SEQ ID NOS: 26
;   SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 479
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-723-368-2

  Query Match             9.5%;  Score 122;  DB 2;  Length 479;
  Best Local Similarity   25.2%;  Pred. No. 0.0013;
  Matches   39;  Conservative   21;  Mismatches   51;  Indels   44;  Gaps    6;

Qy    3 WCLLLIWAQGLRQAPLASGWMTGTETTGNISABKGGSIILQCHLSSTT--AQVTQVNWE 60
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Db   19 WPLLLLL-------LETGAQDVRVQVLPEVRGQLGGTVBELPCHLLPPVPGLYISLVTWQ 71

Qy   61 QQD----QLLAICNADLGWHISPSFKDRVAPGPG------------LG 92
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Db   72 RPDAPANHQNVAAFHPKMG----PSFP--SPKPGSERLSFVSAKQSTGDTEABLQDAT 124

Qy   93 LTLQSLTVNDTGEYFCIYHTYPDGTYTGRIFLEVL 127
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Db  125 LALHGLTVEDEGNYTCEFATFPKGSVRGMTWLRVI 159

RESULT 2
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US-09-949-016-6278
; Sequence 6278, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6278
; LENGTH: 479
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6278

Query Match          9.5%;   Score 122; DB 2; Length 479;
Best Local Similarity 25.2%;  Pred. No. 0.0013;
Matches  39;  Conservative  21;  Mismatches  51;  Indels  44;  Gaps  6;

Qy    3 WCLLLIWAQGLRQAPLASGMMTGTIETTGNISAEKGGSIILQCHLSSTT--AQVTQVNWE 60
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Db   19 WPLLLLLL------LETGAQDVRVQVLPEVRGQLGGTVELPCHLLPPVPGLYISLVTWQ 71

Qy   61 QQD-----QLLAICNADLGWHISPSFKDRVAPGPG----------------------LG 92
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Db   72 RPDAPANHQNVAAFHPKMG----PSFP--SPKPGSERLSFVSAKQSTGQDTEAELQDAT 124

Qy   93 LTLQSLTVNDTGEYFCIYHTYPDGTYTGRIFLEVL 127
          |:|||       :||
Db  125 LALHGLTVEDEGNYTCEFATFPKKGSVRGMTWLRVI 159

RESULT 3
US-09-949-016-7563
; Sequence 7563, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7563
; LENGTH: 522
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7563

Query Match          9.5%;   Score 122; DB 2; Length 522;
Best Local Similarity 25.2%;  Pred. No. 0.0015;
Matches  39;  Conservative  21;  Mismatches  51;  Indels  44;  Gaps  6;

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Qy   61 QQD-----QLLAICNADLGWHISPSFKDRVAPGPG----------------------LG 92
                  ::|     |    :  :
Db  115 RPDAPANHQNVAAFHPKMG----PSFP--SPKPGSERLSFVSAKQSTGQDTEAELQDAT 167

Qy   93 LTLQSLTVNDTGEYFCIYHTYPDGTYTGRIFLEVL 127
          |:|||       :||
Db  168 LALHGLTVEDEGNYTCEFATFPKKGSVRGMTWLRVI 202

RESULT 4
US-09-919-172-20
; Sequence 20, Application US/09919172
; Patent No. 6673545
; GENERAL INFORMATION:
; APPLICANT: Faris, Mary
; APPLICANT: Turner, Christopher M.
; TITLE OF INVENTION: PROSTATE CANCER MARKERS
; FILE REFERENCE: PA-0036 US
; CURRENT APPLICATION NUMBER: US/09/919,172
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/222,469
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PERL Program
; SEQ ID NO 20
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6673545 3189059CD1
US-09-919-172-20

Query Match          8.7%;   Score 111.5; DB 2; Length 518;
Best Local Similarity 24.4%;  Pred. No. 0.016;
Matches  53;  Conservative  33;  Mismatches  84;  Indels  47;  Gaps  11;

Qy    2 RWCLLLIW--AQGLRQAPLASGMMTGTIETTGNISAEKGGSIILQCHLSS--TTAQVTQV 57
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Db   12 RW------WGLALGL-TAFFLPGVHSQVVQVNDSMYGFIGTDVVLHCSFANPLPSVKITQV 65

Qy   58 NWEQ----QDQLLAICNADLGWHISPSFKDRV--APGPGLG-LTLQSLTVNDTGEYFCI 109
          ::    :::|            :::           ::|||
Db   66 TWQKSTNGSKQNVAIYNPSMGVSVLAPYRERVEFLRPSFTDGTIRLSRLELEDEGVVICE 125

Qy  110 YHTYPDGTYTGRIFLEV--------LESSVAEHGARFQIPLLGAMAATLVVICTAV----- 157
          :|:|                    ::::
Db  126 FATFPTGNRESQLNLTVMAKPTNWIEGTQAVLRAK----KGQDDKVLVATCTSANGKPP 180

Qy  158 IVVVALTRKKALRIHSVEGDLRRKSAGQEWSPSAP 194
          ::                              :||
Db  181 SVVSWETRLKGEARVPGDSG----------TPMAP 205

RESULT 5
US-09-949-016-11380
; Sequence 11380, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
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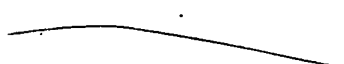
November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions .rnpbm (Published_Applications_NA_Main) and .rnpbn (Published_Applications_NA_New).
Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions .rapbm (Published_Applications_AA_Main) and .rapbn (Published_Applications_AA_New).

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Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- . Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.

- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

  http://www.pir.uniprot.org/database/archive.shtml

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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